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TABEL 1

M							
	00-1	hRSV	bRSV	PMV	APV-A	APV-C	APV-B
00-1	1,00	0,37	0,37	0,37	0,77	0,87	0,75
hRSV	---	1,00	0,91	0,41	0,37	0,37	0,37
bRSV	---	---	1,00	0,42	0,35	0,36	0,35
PMV	---	---	---	1,00	0,37	0,38	0,38
APV-A	---	---	---	---	1,00	0,78	0,89
APV-C	---	---	---	---	---	1,00	0,77
APV-B	---	---	---	---	---	---	1,00
N							
	00-1	hRSV	bRSV	PVM	APV-A	APV-C	APV-B
00-1	1,00	0,20	0,22	0,21	0,40	0,52	0,40
hRSV	---	1,00	0,59	0,30	0,18	0,21	0,18
bRSV	---	---	1,00	0,31	0,21	0,23	0,21
PVM	---	---	---	1,00	0,21	0,23	0,21
APVA	---	---	---	---	1,00	0,42	1,00
APVC	---	---	---	---	---	1,00	0,42
APVB	---	---	---	---	---	---	1,00
F							
	00-1	hRSV	bRSV	PVM	APV-A	APV-C	APV-B
00-1	1,00	0,32	0,33	0,37	0,67	0,80	0,66
hRSV	---	1,00	0,82	0,40	0,35	0,35	0,35
bRSV	---	---	1,00	0,41	0,34	0,36	0,34
PVM	---	---	---	1,00	0,38	0,38	0,39
APV-A	---	---	---	---	1,00	0,72	0,84
APV-C	---	---	---	---	---	1,00	0,72
APV-B	---	---	---	---	---	---	1,00
P							
	00-1	hRSV	bRSV	PMV	APV-A	APV-C	
00-1	1,00	0,25	0,26	0,27	0,55	0,67	
hRSV	---	1,00	0,81	0,30	0,28	0,26	
bRSV	---	---	1,00	0,29	0,28	0,26	
PMV	---	---	---	1,00	0,23	0,27	
APV-A	---	---	---	---	1,00	0,52	
APV-C	---	---	---	---	---	1,00	
L8							
	00-1	hRSV	bRSV	APV-A			
00-1	1,00	0,36	0,35	0,56			
hRSV	---	1,00	0,79	0,36			
bRSV	---	---	1,00	0,35			
APV-A	---	---	---	1,00			
L9/10							
	00-1	hRSV	bRSV	APV-A			
00-1	1,00	0,30	0,30	0,53			
hRSV	---	1,00	0,83	0,34			
bRSV	---	---	1,00	0,32			
APV-A	---	---	---	1,00			

Fig. 1a

Table 2

Seroprevalence of hMPV in humans categorised by age group using immunofluorescence and virus neutralisation assays

Age (Years)	Immunofluorescence assays		Virus neutralisation assays		
	N tested	N positive	N tested	N positive	Titre range
< 1	20	5	12	3	16-32
1-2	20	11	13	4	16-32
2-5	20	14	8	3	16-512
5-10	20	20	4	4	32-256
10-20	20	20	4	3	32-128
> 20	20	20	4	3	32-128
8-99 <sup>1</sup>	72	72	11	11	16-128

<sup>1</sup>Sero-archeological analysis using sera collected in 1958

Fig. 1b

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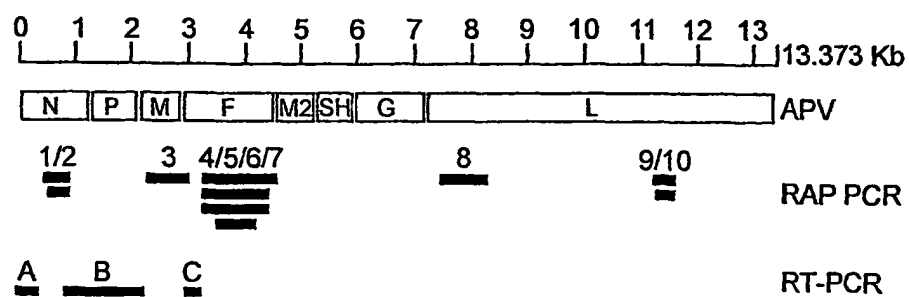


Fig. 2

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Fig. 3

## Nucleo protein

00-1 NP	MSIQGHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQEQETTLGCEILYAKHADYKYAREIGIQXISTALGSSERVQOILANSSEVQVVLRTYSL	10
APV A	...ES.R....E.....ED....R....A...I...E...PQVST...MV.F...T...EP...V.M.....AD.T...K.....G.H.KVIT.	10
APV B	.....Q.....R.VS.....T..SH...V.M..V..T..A..T...K.....A...K....	10
APV C	.....R.VS.....T..SH...V.M..V..T..A..T...K.....A...K....	10
BRV	.A.SKVK.N.TFN.DQL.ST.K...Q.ST.DNIDIPNYDV.KHLNK...ML.ITED.NH.FTGL..ML.AMSR..R.DTLK..KDA.YQ.RANGVDVITH	10
BRV	.A.SKVK.N.TFN.DQL.SS.K...Q.ST.DNIDIPNYDV.KHLNK...ML.ITED.NH.FTGL..ML.AMSR..R.DTLK..KDA.YH.KANGVDITTY	10
PVM	...DRLK.N.V.N.DSL.SNCK.SVT.ST.DV.S.SGHAM.KALARTL.MF.LTAFNRCEEV...L.AMSL..RDSIK...EA.YN.KC.D.QLQDF	10
00-1 NP	GKIKNNKGEDLQMLDIHGVEKSWVEEDKEARKTHATLLKESSGNIPOQRPSAPDTPILLCVGALIFTKLASTIEVGLETTVRANRVLSDALKRYPR	20
APV A	SAEGSVKREVE...N..D.GVG.ADDVERTT.EA.GAMVR.KV-QLTK..K...L.A.V...I.....V.....AI...S.....IS....	19
APV B	..G.S...E.....R..I..V.....SAT.DN..P.....S.A.....I.....A.....N.....F..	20
APV C	..G.S...E.....R..I..V.....SAT.DN..P.....S.A.....I.....A.....N.....F..	20
BRV	RQDV.G.EMKFEV.TLVSLTSEVQGN.EI.S..SYKGM...M..EVAPEY.HDS..CGM.V...A..VI...AGDRS..TAVI...N..RNEI...KG	19
BRV	RQDV.G.EMKFEV.TLVSLTSEIQVN.EI.S..SYKGM...M..EVAPEY.HDS..CGM.I..IA..VI...AGDRS..TAVI...N..RNEI...KG	19
PVM	TTKLGQ.EYKI.V...V.IDAANLADLEIQ..GVV.KE..TG-ARL.D.R.HD...CGV.V..IA..VVS...AGDRG..DAVE...LN..KAEKA...N	19
00-1 NP	MDIPKIARSFYDLFEQVYHRSFLFIYEGKALGSSSTGSKAESLFVNIEMQAYGAGQTMLANGVIARSSNNIMLGHVSQAEKQVTEYVDLVREMPESG	30
APV A	...R..K..FE...K...Y.N.....T...RM.....R..S.....K.....	29
APV B	I.....Y.....	30
APV C	I.....Y.....	30
BRV	LIPKD..N...EV..KYPHYIDV.VHF.I.QS.TRG..RV.GI.AGL..N...V...L.K.VK...A...ME..V...EYAKQL.G.A.	29
BRV	LIPKD..N...EV..KHPHLIDV.VHF.I.QS.TRG..RV.GI.AGL..N...S..V...L.K.VK...A...ME..V...EYAKQL.G.A.	29
PVM	EVKQ..E.....R.P.YIDV..TF.L.QS.VRG...V.G..SGL..N...V...LL.K.VK...A...ME..V...EYAKQK.G.A.	29
00-1 NP	LLHLRQSPKAGLLSLANCPNFASVVLGNASGLGIIMYGRVNPTELSFAESYAKSLKESNKNFSSGLTDEEKAAEHFLNDDSDNDYE	39
APV A	.....T.....A.....K..A..L..A.....RT.R.N...LAA...D.R...TSY.GGD.ERSKF.	39
APV B	...N.....L.....A.....R.....N...INEEG....	39
APV C	...N.....L.....A.....R.....N...INEEG....	39
BRV	FY.I.LNN...S...TQF...S.....A...M.E...TPR.QD.YD..KA..EQ...NGV..Y.V.D..T..L..IKNQ..PK.N-DVEL	39
BRV	FY.I.LNN...S...TQF...S.....A...M.E...TPR.QD.YD..KA..EQ...NGV..Y.V.D..A..L..IKNQ..PKE.-DVEL	39
PVM	FY.I.LNN...S...T...T.....A.....S.K.APR.R...D..KD..ER..DN.V..Y.A.N..A..R.LISQO..IV..TPD.DI	39

## Phospho protein

00-1 P	MS-FPEGKDILEFMGNEAAKLAFA-----QKSLRKPGHKRSQSIIGKVNVTSETLEPTISRPAKPTIPSEPKLAWTDGKGATKTEIKQAIVMDP	91
APV-A	...M.S...M.D.Y-----R...NTSAG-GR..S..PI..IA.KVP..PLCN.TT-----SCI..PKAFVP..K--	76
APV-C	...L.....A.....R..K.I..R.T...V.D.II...V.K...KST.V.T.P.R.N..GE.PDT.RSQTEE.RNEAT.	91
BRV	-----	80
BRV	.EK.APE-----H.ED.NNK.TK.LES-----IKGKF-----ASSKDPKK.DS.ISVNS	45
PVM	.EK.APE-----V.ED.N.K..E.LKHSFPPE.P.AGIPNTATHVTKYNNMPPILRSSEK..SPRVA.NL.E.A.A-----PTTTPP.PPQN.EEQPKESD	92
00-1 P	IEEEESTEKVLPSSDGKTPAEKKLPSTNT-----KKKVSFTNPEP-----GKYTKLEKDALDLSNDEEEDAE-SSILTTEE-RDTSSLSIEARLESIE	18
APV-A	---I...IYP.LPTAPVATDTYTSTSTE.AKK-----S...K.DNPKV-----EEG.E...P..DND.K.....K..A.T.....A..	16
APV-C	EDASRLY.EVEA.T.....GKETPEKP-----T.KND.S---R....ME..E.....DD...-V....-K...A..L.....D	18
BRV	-----	16
BRV	.DI.VTK.SPITSGTNIIN.TSEADSTPETKANYPR.PL...KEDLTSPDNPF.S..Y.ETIETF---DNN---EE.SYSY..INDQ.-NDN.T...DR.D	13
PVM	VDI.TMHVC...PONPEHSKKPCCSDDT.D.KKT---R.PM.T.VEP.EKIV.LGAS.YRETMQTF---AADGYDEE.N.S...TNQEPG.S.V.Q..DR..	18
00-1 P	EKLSMILGLRLTINIATAGPTAARDGIRDAMIGVREELIADIKEA---KKGAEAM---MEEEMXORSKIGNSGVKLTEKAKELNKVDESTSGESEE	27
APV-A	.....M.K.....M.....NS.MT...---D.I...---K..DT..A...D.....L..Q.S.....S.	25
APV-C	.....V.....V.L.....---K..AK.K.....G.....	27
BRV	-----X-----	26
BRV	...E...M.H..VV.S...S.....V.L..H.EK.RA..LMTNDRLEA.ARLRN..SERMA.DTSOE.P.NPTS.K.SDLL..N-----	23
PVM	...Y.I...N.IMV.....T...E...L..T...EM.KSDILTVDRIVA.EKLRD..CSRADTDGGSACY..DR.RI.D...SSNA-----	27
00-1 P	EEPOTQDQNSQEDDIY---QLIM.	29
APV-A	..SGESESDEE.S...NLDL-L	28
APV-C	..EE.EEESNPD..L.SLTM-LIKN	29
BRV	-----	28
BRV	---.SDNDLSL.-----DF.	24
PVM	---EEAKEDLDV...MGINF-LI	29

## Matrix protein

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Fig. 3, contd.

00-1 matrix	MESYLVDYTYGPIPTAAVQVLEKDLPLASLTITWFLPQANTPPAVLLDQLKLTITTTLYAASONGPIKVNASAGQARMFVLPKKFEVNAVYXDEYS	10
APV-B	...II...V...NN...K...V...SS...AP...S...Q.TV.PE...V.Q...T...SA...S.S.AA.L...L...	10
APV-A	...II...V...SN...T.V...SS...AP...S...Q.TV.PE...V.Q...A...SA...S.S.AA.L...L...	10
APV-C	...V...T.V...Q...R...V.V...T...T...E...T...T...SA...S.D.S.S.L.D...L...	10
hRSV	...T.VNKLHE.ST...YNV...DO...V.M...SSISADL.IKE.INVN.LVRQISTLK.S...IMNSRS.VLAQM.S...TIS.N.SL...R...	10
hRSV	...T.VNKLHE.ST...YNV...DO...V.M...SSV.ADL.IKE.ASIN.LVRQISTPK.S...R.TINSRS.VLAQM.SN.IIS.N.SL...R...	10
PVM	...A...EM.H.V...LN.V...HSANI...V.I.M...TSL.KNSVM.L.HDV.VICTQISTVH...MI...DL.SSN.GLAM.RQ.LI...II.L.DWG...	10
00-1 matrix	KLEFQKLTVCVKTYVLTTPKPYGRVSKFVSSAKSVGKTHDLIALCDFMLEKNTPTVITPAFIRKSVIKESSESATVERAIISSADQALQAKIAPYAGL	20
APV-B	...D.GV...D.RA...L...I.TMNT...R...I.M.RGI...Y.A...D...G...I...R...	20
APV-A	R...GT...D.RSI...L...DMDVR...R...I.I.GV.I...Y.A...D...G...I...R...	20
APV-C	...L.A...N...A...L...GV...Y...I...R...	20
hRSV	...AY.IT.P...I.ACS...CL.VKN.LTTVKDLTKTNP...EI...E.ENIMTSKR.V.T.LR.INV.AKOLDSL.NIATT.FKN.I.N...I...	20
hRSV	...AY.VT.P...I.ACS...CL.VKS.LTTVKDLTKTNP...EI...E.ENIMTSKR.I...TYLAPI.V.NKOLDSL.NIATT.FKN.I.N...I...	20
PVM	NMDYEVVPAFDK.SFCV.LL...KN.LYTVP.ITPTN-RP...E...V.S.HNRVTLSEN...V...RALY.RQGLDS...Q...DV.H.I.T.RV...	19
00-1 matrix	IMIMMNNPKGIFKKLAGTQVIVELGAYVQAESISKICKTWSHQTRYVLSR.	25
APV-B	...L.A...R...P...LG...N.R...I...L-K-SR	25
APV-A	...L...M...P...LG...N.R...R...GYPK-A.-IC.C-YSQ.K	25
APV-C	...V...R...RN...R	27
hRSV	VLVI.VTDN...A.YIKPOS.F.D...LEK...YVVTN.K.TA.KESI.P...IED.	25
hRSV	VLVI.VTDN...A.YIKPOS.F.D...LEK...YVVTN.K.TA...FSI.P...IED.	25
PVM	TLVINITST...A.L.K.S.ILA...P.LTQV.LHDVIMN.K.T.S.I...SS...TSG.	25

## Fusion protein

00-1 F	MSW---KVVIXFSLI---TPKHGLKESYLEESCSTITEGYLSVLRTGWYINVTLEVGDUENLTCDGPS---LIKTELDTLSALRELATVSADQ	88
APV-A	.DV---RICLLF.IS---N.SSCIQ.T.N...V.R...K...N.I.N...I.N...D...V...N...K...88	88
APV-B	.YL---LLLIY.VV---GASGKIQ.T.S...V.R...K...N.I.N...I.N...S...S...QN...Q...88	88
APV-C	...LLLV.A---TG...E...Y.V.R...T...R...E...N...E...K...88	88
hRSV	.ATTAMRI.SIIFISTYVTHI.LQONIT.EFYQST.AVSR...A...S.V.I.LSKIQKNV.KSTD.KVK...Q.ERYNN.VV.QSLMONE	10
hRSV	.ELLHRLSAI.LT.AINRLYL.SSONIT.EFYQST.AVSR...F.A...S.I.I.LSNIKETK.NGTOTKVK...Q...KY.N.VT...QLLMONT	10
PVM	---IPGR.FLV...VIFNTKPIHNT.T.K.Y.ST...VE.A...K.A...RMT.MSILSQIMIES.KSSN...LAH...AIYS...VD...L.SNA	93
00-1 F	LAREEQ---IENPQSRFVLGAIALGVATAAAGVATIAKIRLESEVTAIKNAIKKINEAVSTLNGVRVLATAVRELK	16
APV-A	V.K.SR---LSS...RR...L...G...K...RN...ND...16	16
APV-B	ITK.NR---LSH.KK...T...L...G...K...L.RS...I...ND...16	16
APV-C	.K.AR---MS...KA...G...A...G...R...ND...16	16
hRSV	P.SFSRAKRGIPELIHYNTRNKKFYGLMGKK.KR...L-GEL...IG-S...AS...VS.VLH...G...NK...LS...K...VS...S...TSK.LD...19	19
hRSV	P.ANNRRAREAPQYMYNTINTTKNLAVS.SKK.KR...L-GEL...G-S...IAS.I.VS.VLH...G...NK...LS...K...VS...S...TSK.LD...19	19
PVM	---LKSK.KK...L-GLI...LG...L...VQ...IAL.RD.VRN...VS.T.MS...RV.DD...16	16
00-1 F	DEVSKNLTRAINKNCIDIALRMVAFSFSQFNRRFLAVVRQFSDNAGITPAISLDLMDAELARAVSNMPTSAGQIKIMLENRAMVRKGFGLIGVYSS	26
APV-A	E.I...K...P...Q...N...I...G.N...S...S.V...D.V...INR...S...S...N...I...DGT	26
APV-B	E.I...K...P...Q...N...IR...I...G.N...S...S.V...VK...INR...S...S...N...I...GT	26
APV-C	.I...K...P...R...S...G.Y...V...V...S...N...I...26	26
hRSV	NYID.E.LPQV.NHD.R.SNIETVIE.Q.K.N.L.EIA.E.V...TPL.TYML.NS...LSLIND...ITND.K...SS.VQI...QQSYSIMSV.KEEV	29
hRSV	NYINNO.LPQV.QQS.R.SNIETVIE.Q.K.S.L.EIN.E.V...V.TPL.TYML.NS...LSLIND...ITND.K...SS.VQI...QQSYSIMSV.KEEV	29
PVM	N.I...E.LPK...RVS...VH.ITAVIR.Q.L.K.L.E.S.E.S...L.HTV.SPML.R...TSI.GG.AV...KEI...SSK.IM...N.LAI.SS.NADT	26
00-1 F	VDMVQLPFVIGVIDTPCHIVKAAPSC---SGKGNVACLLREDQGWYCNAGSTVYYPNEKDCETRGDHFVFCUTAGINVAEQSKECNINISTINYCKVS	36
APV-A	.VY...E...R.V...L---RKE...I...T...A...KD...V.D.Y...LEVEQ...Y...SK...36	36
APV-B	.VY...E...R.V...L---RHERES...T...A...D...V.D.Y...SEVEQ...H...ST...36	36
APV-C	.VYI...K...L---D...E...V.S...KE...E...R...K...36	36
hRSV	LAYV...Y...KLHTS.L.TTND.E.SNI...T.T.R...D...VSFF.QDET.KVQSNR...MNSLTLPDVLN...TD.FN.K.D...IM	39
hRSV	LAYV...Y...KLHTS.L.TTNI.E.SNI...T.T.R...D...VSFF.QDET.KVQSNR...MNSLTLPSEVSL...TD.FNSK.D...IM	39
PVM	LVIYI...L...M...D...VIRSSID---HNIADK...A.A.N...H...LS.F.SPT...IHNGYA...LKSILT.PVT.R...S.MY...D...I...35	35
00-1 F	TGRHPISNVALSPGLAVACYKGVSCSIGSNRVGILKQKNGCSYITNQADVTIDNTVYQLSKVEGEQHVIGKRPVSSSFPDKFFEDQFNVALDQVF	46
APV-A	...V...T...G...S...ES...K...G...TH.P.NE...I...V...RT...A...VNN.N.I.L...46	46
APV-B	...V...T...G...S...E...K...G...TH.P.NE...I...V...RT...A...VNN.N.LL...46	46
APV-C	...D...M...K...RP.G...S...T...K...N...IE...I...46	46
hRSV	.SKTD...SSVITSI...I.S.GTKT.TASNKOR...TFSN...D.VS.KGV...SVG...L.YVN.L...KALY...E.IINY...LV...S.E.DASIA...N	49
hRSV	.SKTD...SSVITS...I.S.GTKT.TASNKOR...TFSN...D.VS.KGV...SVG...L.YVN.L...KNLYV...E.IINY...LV...S.E.DASIS...N	49
PVM	.SKTYV.TAV.TTM.C...S.GHN...TVIN.DK...RT.PD...H...S.KGV.R.QVG...Y...EV.KSI.VR.E.LVLAY...LS...D.K.D...IRD.E	45
00-1 F	ESIENSQALVDQSNRIIS---SAEKGNTGFI---VIIILAVLGSIMLLVSFIIKKTKRPTGP-PELSGVITNNGFIPH-N.	54
APV-A	...DR...D.I.K...DL.G---ADA.SKA.IA---A.VVLVI...I.FFLAVIYYCSRVR.TKPHDY.ATT.HSSAYV---S	53
APV-B	...VDK.KD.I.K...DL.D---IEV.S.I.AAL---A.TILV...SLIL.VGLIAYVV...R.AK.SNGY.KIT.QS.M.Y.S.	53
APV-C	...V.K.N.I...K...D---I...A.V...V.VL.MLAAGV.G...FVV...R.AAPKF...M.MN...N.K...-F.LLAKKKKKKKK	55
hRSV	AK.NQ.L.FIRR.DEL.H---SVDVG.ST.NVV.TTI...V.V.VIHL.A.GLLFYC.TKST.IMLQKD...IN.LS.S---K	57
hRSV	K.NQ.L.FIRR.DEL.H---NVNTG.ST.NIM.TTI...V.I.VLSSL.AIGLLLYC.AKNT.VLSKQD...IN.IA.S---K	57
PVM	H...NQRTRFFKA.DQL.DLSENREN.NLANSY.LTTLLEVM.III.AVIGFLYKVLK---MIRDNK.KSKSTP.IT---VLS	53

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Fig. 3, contd.

## L polymerase RAP PCR fragment 8

00-1 fragment 8 -----TVNVLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVIEHVRILKNAVNSKMKISDYK-----IVEFVNQHE 77  
 APV-A ME-ISNESV.....V.N...I.D.Y..H..MT.....Q..RALFK.LTISRE.R-----V...LMT.K. 84  
 bRSV MDTLIHENST...T.....C..L..Y..DG.....Y.NIISRQK.L...IN..KLSIIQSFVTK.NKGELGLE..TYF.SL 90  
 hRSV MDPIINGNSA...T.G.....C..L..YIFNG.....Y.NLISRQ..L...MN..KINITQSL..K.HKGEIKLE..TYF.SL 90

00-1 fragment 8 IM-KNVHSCEL-TLLKQFLTRSKNTSLKLANMICDWLQK-----STSDOTSILSFIDVEFI----- 13  
 APV-A LL-VAAGAR-----KK..KW.G...D..EV..K.VT...K.S-----Q.PGRGK.IDR.Q..NL 13  
 bRSV L.TY.SLSTS..ITTT..F.KIIR.AIE..DV.VYA.LNK.G..EKGKVDRC-DDTN.TLSNIVRDNLSVLSDNTPSTKKPNSSCK 17  
 hRSV L.TY.SMT.S.QIATTN...KIIR.AIE..DV.VYA.LNK.G..EKDKKSNNGQDE.NSV.TTI.KDILSAVKDNQSHLAKADKHSTK 18

00-1 fragment 8 -----PSWVSNWFSNWNLNKILILEFRKEEVIRTSIL-CRSLGKLVFVSSYGCTIVKSNKSKRVSFPTYNQLL 20  
 APV-A -----D.LEH..DS.LI..DV.QSY.CL..SQ.SA..-RK.SLNEF.A...F...II.R..R.IC.C..... 20  
 bRSV PDQPIKTTILCKLLSSMSHP.T.LIH..NLYTK..DILTQY.TN.ARNH.Y..IDT.T..EFQ.IINQ.....YHK.L.KITIT....F. 26  
 hRSV QKDTIKTTLLKQKMSQHP...LIH..NLYTK..NLTQY.SN..KNH.FT.IDNQT.SGFQ.IINQ.....YHKEL..ITVT....F. 27

00-1 fragment 8 TWKDVMLSRFNANFCIWWVSNLNEQSGVGLASNL-----Q 23  
 APV-A ....LA.....L.V....C..SA.D.L....K.VGELLNR 24  
 bRSV ....IS...L.VCMIT.I..C..TLNKS...C 30  
 hRSV ....IS...L.VCLIT.I..C..TLNKS...C 30

## L polymerase RAP-PCR fragment 9/10

00-1 fragment 9/10 --KLVDKITSQHFSPDKIIMLTGLKMLMP--TIKQKTDQ-----FLNKRENYFHCNLIIESLSAALAXEWCILTEQC 72  
 APV-A -F.S.R..VT.....N..H..LVM...L.L.--VRSNINNN-----KPAT..F.N...IV.A.TSC..C...TV.IILT 72  
 bRSV -ICKINQVIQK..M.L....SLSQYVELFLSNK.L.NSPHISSNLVLVH.MSD..LHKYV---.TN..G..IM.IQIMK 76  
 hRSV DIHKLKQVIQK..M.L....SLSQYVELFLSNK.L.SGSHVNSNLILAH.ISD...NTYI---.TN..G..IL.IQIMK 77

00-1 fragment 9/10 IENNIFFKDWGDFISDHFMDPKIFLCVFETKILC 10  
 APV-A T..S..Q.E.....T....IN.TW..MS...Y...HW 11  
 bRSV DSKG..E....E.Y.T..M.L.LNV.FDAY..Y. 11  
 hRSV DSKG..E....E.Y.T..M.LNV.FDAY..Y. 11

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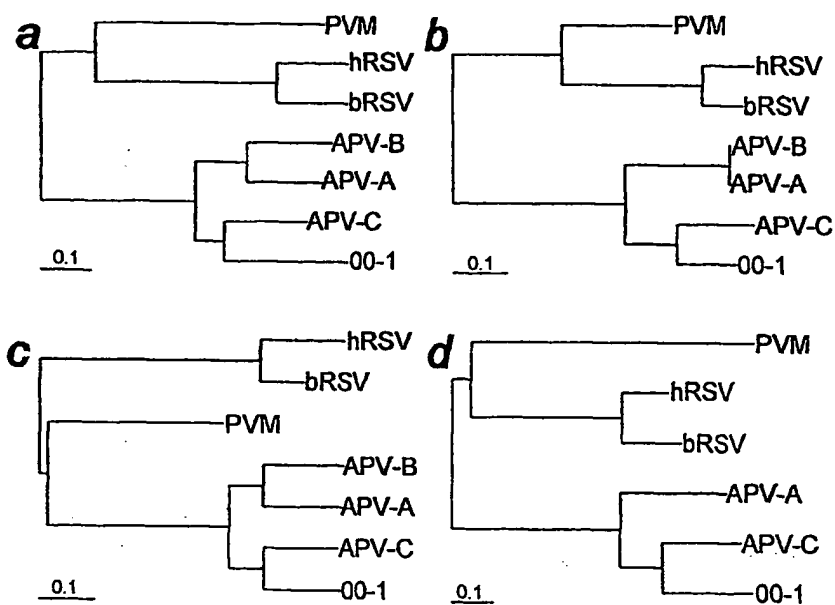


Fig. 4

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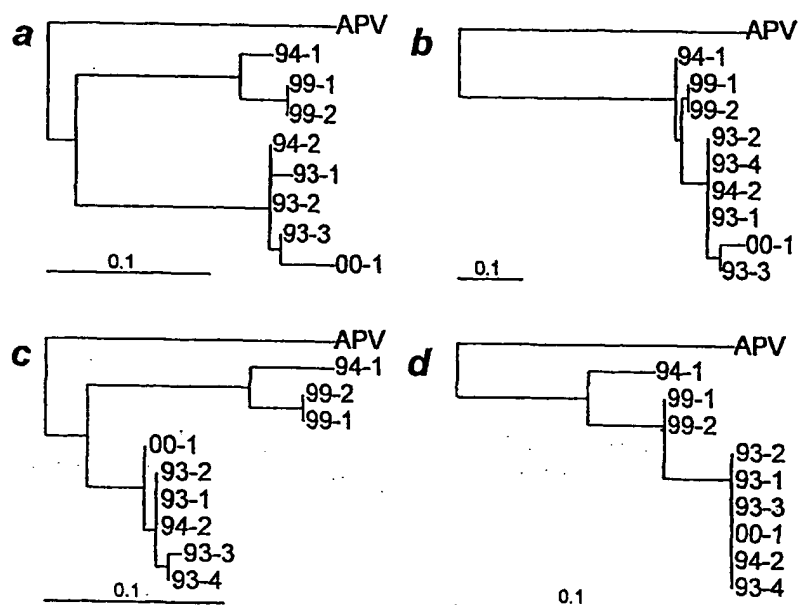


Fig. 5



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**Fig. 6A**

160  
ACGCGTATTAATGATGATCAAAAGATATGGGCAAGATGCTCTTCCTCAAGGGATTCACCTGAGGTATATATACACAGCATGCTATATTAAGAGGTCTCAGTACACAAATTAAGAGAGATGTCGGGTACACCACTGCGATGACA

170  
H G Q V K H S L Q G I H L S O L S Y K H A I L K E S O Y T I K R D V G T T Y A V T

180  
CCCTCATCTTGCACAAAGAAATACACTGTTGTGTGGAGAAATCTGTATGCTTAACATGCTGACTACAAATATGCTGCCAGAAATAGGATACAAATATATAGCACAGCTTTAGCATCAGAGAGATGTCACCGATTTCTGAGCACTCA

190  
P S S L O O E I T L L C C E I L Y A K H A D Y K Y A A E I G I Q Y I S T A L G S E R Y Q O I L R N S

200  
GGCAGTAGGTCCAGTGCTCTTAACCCAGACACTGCTCTGGGGAATAATTAAGAGAGATTTACAGATGTTACAGATACACGGGTAGAGAGAGCTGGGTAGAGAGAGATAGACAAAGAGCAAGGAAACATGCGA

210  
Q S E V O V V L T R T Y S L G K I K N M K G E D L O M L O I H G V E K S W V E E I D K E A R K T M A

220  
ACCTTGTAAAGGATCATCAGGTAAATCCCAACAAATCAGGGCCCTCAGCAGCAGACACACCAATATCTTATATGCTAGGTGCTTAAATTCCTAACTAACATAGCATCAACCATAGAGATGGGACATAGAGACCACTCAGAGG

230  
T L K E S S G N I P O N O R P S A P O T P I L L C V G A L I F T K L A S T I E V G L E T T Y R R

240  
GCTAACCGTGTACTAAGTGAATGCATCAAGATACCTTAGAATGGACATACCAAGATGCTCTATGACTTATTTGAACAAAAGTGTATACAGAGATTTGTTCATTGAGTATGSCAAAGCATTAGGCTCATCATCTACA

250  
A N R V L S D A L K R Y P R H D I P K I A R S F Y D L F E O K V Y H R S L F I E Y G K A L G S S T

260  
GGCAGCAAGCAAGATCTATTTGTAAATATATATCAAGCTTATGGGGCCGTCACAACTATGAGGTGGGGGCTATGCCAGGTCTATGAGCATCAATATATGTTAGGACATATATGCTCCAGCTGAGTTAAACAGCTGACA

270  
Q S K A E S L F V N I F M O A Y G A G O T M L R W G V I A R S S N N I M L G H V S V O A E L K O V T

280  
GAAAGTCTATGACTTGTGGAGAAATGGGGCTGMACTGAGACTCTCTACATTTAAGGCAAGGCTCCAAAGTGGACTGTATATCATAGCCAGCTTCCCACTTTGCAAGTGTGTGCGAAATGCTTCAGGCTTAGGCTAATTCGT

290  
E E V O L Y R E H G P E S G L L H L R O S P K A G L L S L A N C P N F A S V V L G N A S G L G I Q

300  
M Y R G R Y P N T E L F S A E S Y A K S L K E S N K I N F S S L G L T D E E K E A E A E H F L N V S

310  
GAGCAGCAGTCAAAATGATATGAGTAAATTAAGAGTGGGCAAGTCAATGTCTTCCCTGAAGGAAGATATCTTTTCATGGGTATGAAGCAGCAAAATAGCAGAACTTTCCAGAAATCATTAAGAAACCCAGGTCTATAAA

320  
D D S O N D Y E . H S F P E G K O I L F H G N E A K L A E A F O K S L R K P C H K

330  
GAGTCTAATCTATATAGGAAAGATGAATCTATCTACAAAGATTCGAATTAAGTACTACTATCTAGTACACTGCCAAACCACTACCTGTCAGACCAAGTAGCATGAGAGATTAAGGTGGGGCAACCAAACTGAAATTAAGC

340  
R S O S I I G E K Y N T V S E T L E L P T I S R P A K P T I P S E P K L A W T D K G G A T K T E I K

350  
AAGCAATCAAGTATGGATCCCATTTGAAGAGAGAGCTTACCGAGAGAGGTGCTACCTCCAGTATGGAAACCCCTGCAGAAAGAAATGAAACCATCACTACCAACCAAGAGGTTCATTTACACCAAAATGACAG

360  
O O A I K V H D P I E E E S T E K K V L P S S O K T P A E K K L K P S T N T K K K V S F T P N E P

370  
GGGAAATATACAAAGTGGAAAGATGCTCTAGATTGCTCTCAGATATGAAGAGAGAGATGCAAGATCTCAACTTAACTTTGAAGAAAGAGATCTCTCATCATAGCATTCAGCCCATGGAATCAATAGAGGAGAAATTA

380  
Q K Y T K L E K D A L D L S D N E E D A E S I L T F E E R D I S I S I E A R L E S I E E K L

390  
GSCATGATATAGGCTATTAGAACACTCAACATTTGCTACAGCAGGAGCCACAGCAGCAGAGATGGATGCAATGATTTGGCGTAAAGAGGAAATTAATAGCAGACATAATAGAGAACTTAAGGAAAGCAGCAAAATGA

400  
S M I L G L L R T L N I A T A G P T A A R D G I R D A M I G V R E E L I A D I I K E A K G K A A E H

410  
TGGAGAGGAAATGAKTCAACGATCAAAATAGGAATGGTATGTAATTAACAGAAAGCAAGAGAGCTCAACAAATTTGTAAGATGAAGCACAAGTGGAGATTCGGAAGAGAGAGAAAGCAAGAAAGCAGACAGCAATA

420  
M E E M 7 O R S K I G N G S V K L T E K A K E L N K I V E O E S T S G E S E E E P K D T O D N

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Fig. 6A, contd.

225C GTCAAGAAGTACATTTACCGATTAATATGATTAATAAATAAACAATGAGCAATGAGTCTACCTAGTAGACACCTTCAAGGCACTTCCTTACACATGACAGTCTTCAAGTGTGATCTAATAGAAAAGGACCTGTT  
240C S O E D D I T Y Q L I M P GS GE H E S Y L V D T Y D G I P Y T A A V D V D L I E K D L L  
ACCTGAAGCCTAACAAATATGGTTCCCTTTGTTTCAGGCCAACACACACCAGCAGTGTCTGATACCTTAACAAACCTGACAAATACCACTCTGTATGCTGATCACAATAATGCTCAATACTCAAAAGTGAATGTCATCAGCCCAAGG  
250C P A S L T I V F P L F O A N T P P A V L L D Q L K T L T I T T L Y A A S Q N C P I L K V N A S A Q G  
TGCAGCAATGTTGTACTTCCCAAAAATTTGAAGTCAATGCCACTGTAGCAATGATGATATAGCAAACTGCAATTTGACAACTCAGAGTCTGCAAGTAAACACATTAATTAACAACTCAACCAATCAACCAATACCGGATGATCAAA  
265C A A M F V L P K K F E V N A T Y A ? D E Y S K L E F D K L T Y C E V K T V Y L T T M K P Y G M V S K  
ATTTGTGAGCTCAGCCAAATCAGTTGGCAAAAACACATGATCTAATGCCACTATGTGATTTATGATCTAGAAAAGAACACACACCTGTACATACCAAGCAATTCATCAATCAGTTTCAATCAAGAGAGTGAATCAGTCTGTTGA  
270C F V S S A K S V G K K T H D L I A L C D F H D L E K N T P V T I P A F I K S V S I K E S E S A T V E  
AGTGTCTATAGCAGTGAAGCAGACCAAGCTCTAACACAGGCCAAATTTGCACCTTATGCGGATTAATATGATGACTATGAACAAATCCCAAGGCAATATTCAAAAGCTTGGAGCTGGAGCTCAAGTCAATGATGATAGTAGGAGC  
285C A A I S S E A D O A L T O A K I A P Y A Q L I M I M T M N P K G I F K K L G A G T O V I V E L C A  
ATATGTCCAGCCTGAAGCAATAGCAAAATATGCAAGACTTGGAGCCATCAAGGAGCAGATATGCTTTGAAGTCCAGATTAACCAAGCAGCTTGGCCAGAGCTTACTAACCTTATCTCATAGATCATAAAGTCAACCAATCTTAGTTAT  
300C Y V O A E S I S K I C K T W S H O Q T R Y V L K S R GE  
ATAAAATCAAGTTAGAACAGATTAATCAATCAAGAGCAGCAATTAATAATGCTTTGAAAGTGGTGAATCTTTTCATTTGTTAATACACCTCERACAGCTTAAAGAGAGCTACTTAGAGAGCTACTAGTATGACTATAACT  
315C GS GE H S W K V V I ? F S L L I T P ? H Q L K E S Y L E S C S T I T  
GAAGTATCTCAGTGTCTCAGCAGCTTGTACCAATGTTTTCACACTGGAGTAGGATGATGAGAGCTTACATGTGCGGATGAGCAGCTTAATAAAGAGAGATTAAGCTTGAACCAAGCTTGAAGAGCTCA  
330C E G Y L S V L R T G W Y T N V F T L E V C D V E N L T C A D G P S L I K T E L D L T K S A L R E L R  
ACAGTTTCTGCTGATCACTTGGCAAGCAGAGCAGCAATTAAGAAATCCAGACAACTAGATTCGTTAGGAGCAATAGCAGCTCGGTGTGCAACTGCACTGAGAGAGCTGAAAGATTTTGTGAGCAGAGATCTAACAGCTGCAATCAACAAACCAAGTGC  
345C T V S A D O L A R E E Q I E N P R O S R F V L G A I A L G V A T A A A V T A Q V A I A K T I R L E S  
GAAGTAACAGCAATTAAGATGCCCTCAAAAAGACCAATGAAGCAGTATCTACATTTGGGAAATGGAGTTGTTGGCAACTGCACTGAGAGAGCTGAAAGATTTTGTGAGCAGAGATCTAACAGCTGCAATCAACAAACCAAGTGC  
360C E V T A I K N A L K K T M E A V S T L G N G V R V L A T A V R E L K D F V S K N L T R A I N K N K C  
GACATTCCTGAGCTGAAAAATGGCCGTAGCTTCACTCAATTCACAGAGAGTTCTTAATTTGTGCGCAATTTTCAGACACCTGCAATTAACACCAAGCAATTAATGACAGATGCTGAACTAGCCAGAGCTGTTTCC  
375C D I A D L K M A V S F S Q F N R R F L N V Y R Q F S D N A Q I T P A I S L D L H T D A E L A R A V S  
AACATGCCAACATCTGCAGCAAAATAAACCTGATGTGGAGAACCTGCAATGATGAGAGAGCAAGGCTTGGAGTTCTCTGATAGGATTTACGGAAGCTTCCGTAATTTACATGCTGCAACTGCAATCTTTGGGTTTATAGACAGCT  
390C M P T S A G O I K L M L E N R A M V R R K Q F G F L I G V Y Q S S V I ? M V Q L P I F G V I D T P  
TGTGATAGTAAACAGCCCTCTTGTTCAGGAAAAGGGAAGTATGCTTGGCTTTAAGAGAGAGCAAGGATGATTTGCAAAATGCCAGGCTCACTGTTTACTACCAATGAAAAGAGCTGTGAACAGAGAGAGACAT  
405C C V I V K A A P S C S G K K Q N Y A C L L R E D O G W Y C O N A G S T Y Y P N E K D C E T R G D H  
GTCTTTGGCAGACAGCAGGAATCAATGTTGCTGAGCAGTCAARGAGTGCACATTAACATATCTACTACTAATACCAAGTASCAGAGAGAGCACTCTATCAGTATGTTGCACTATCTCTCTTGGGCTTGTGTT  
420C V F C D T A A G I N V A E O S ? E C N I N I S T T N Y P C K V S T G R H P I S H V A L S P L G A L V

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**Fig. 6A, contd.**

[illegible]

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CAGCAAAAACAGTGTCCCACTGGTTAATGTCATCTCTCCAGCTCATATCTTAAAGAGAGTAATTCCTTTAGTAGAGTAATGCAATTTGGTTCATGTCTCTTAAAAAGACCTTACCTTAAAAAATGACACACACTGCAAAAGATTGCCATAGAG 16C  
 Q E K N C S T V N V Y L P D S Y L K G V I S F S E T N A I G S C L L K R P Y L K N D N T A K V A I E  
 AATCTGTATCGAGCATGTAGACTCAAAAATCGCAGTCAATCTTAAGATGAAATATACAGATTACAGATAGTAGAGCCAGTAACATGCAACATGCAAAATTATGCAAGAAATGACACAGTTGTGAGCTGCACATTAATAAACAGTTTTTA 30C  
 N P V I E H V R L K N A V N S K H K I S D Y K I V E P Y N M O H E I M K N V H S C E L T L L K O F L  
 ACAGCAGTAAAAATATTAGCACTCTCAAAATTAATATGATATGTGATGTGGCTGCAGTTAAAGCTACACATCAGATGATACCTCACTCACTTAAGTTTATAGATAGTAAGTTTATACTAGCTGGGTAGGCAATTTGGTTTACTAATGGTAC 46C  
 T R S K N I S T L K L N H I C D W L O L K S T S D T S I L S F I D V E F I P S W V S N W F S N W Y  
 AATCTCAACAAGTGTATCTGGAATTCAGBAAAACAGACAGTAAATAGAACTGGTTCAACTCTGTGTAGCTCATTTGGTAAATTAAGTTTGTGTATCATCATATGGATGTATAGTCAGAGCAACACAAAGCAAGAGTGCCTCTTC 60C  
 N L N K L I L E F R K E E Y I R T G S I L C R S L G K L V F V V S Y G C I V K S N K S K R V S F F  
 ACATACATCACTGTACATGGAAGATGTGTGTTAAGTAGATTCAATTCGAAATTTGTATATGGTAAAGCAACAGCTCTGAAATCAAGACGGGTAGGGTTGACAGAGTAATTTGCAAGGAGCATTAATTAACATAAGCTATAT 76C  
 T Y N O L L T W K D V M L S R F N A N F C I W V S N S L N E N O E G V G L R S N L O G I L T N K L Y  
 GAAACTGTAGATTATAGCTAGTTTATGTT 781  
 E T V D Y M L S L C

**Fig. 6B**

ATAGCTAGTAAAGTAACCTTCGTATCAACATATCTCAGTCACACAAAATAGATATGTTAACTACCTGGGAAAAATGCTCATGCGCCAACTATAAAGGTCACAGAAACAGATCAAGTCTGTAACAGAGAGAGAAATATTTCCTATCGGA 15C  
K L V D K I T S D Q H I F S P D K I D M L T L G K M L M P T I K Q Q K T D D F L N K R E N Y F H G

ATAATCTATTGAGTCCTTGTGCACGCTAGCATGCTGCTGTGGCATATTAAACAGACCAATGTATAGAAAATAATATTTTCAAGAAAGACTGGGGTCACGGGTTCATATCGSATCATGCTTTTATGGAGCTCAAAAATTCCTAT 30C  
N N L I E S L S A L A C H W C G I L T E Q C I E N N I F K K D W G D G F I S D H A F M D F K I F L

GTGCTTTTAAACCTAACTTTTATGTA 327  
V F K T K L L C

**Fig. 6C**

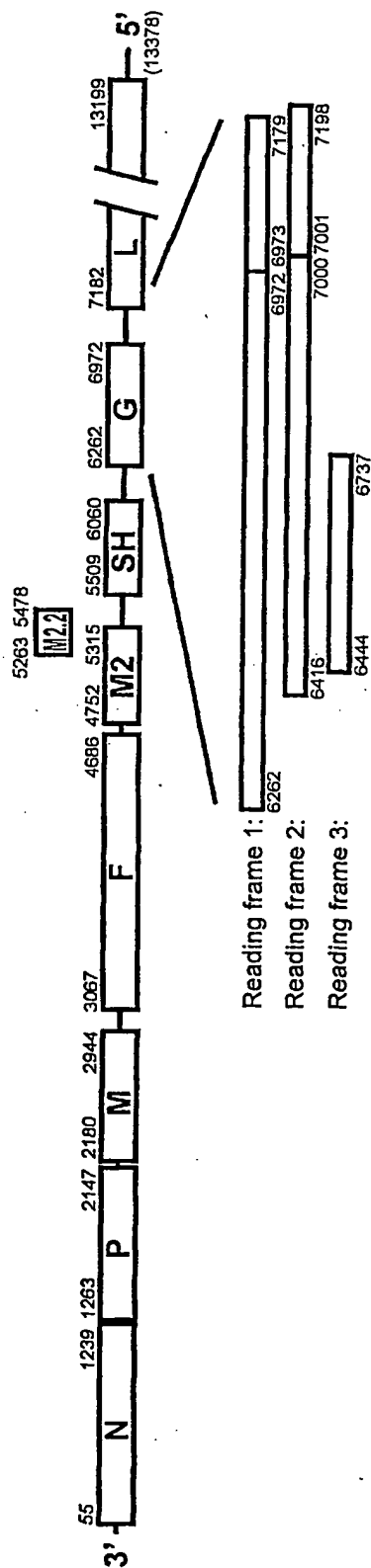


Fig. 7

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Fig. 8

50  
HMPV MSLQGIHLSDL SYKHAILKESQYTIKRDVGT TTA VTPSSLQOEITLLCGE  
APVC .....Q.....R.VS.....  
APVB ...ES.R...E.....D.....R...A...I...E...PKVST...M  
APVA ...ES.R...E.....ED.....R...A...I...E...PQVST...M  
HRSVA .A.SKVK.N.TLN.DQL.SS.K...Q.ST.DSIDTPNYDV.KH.NK...M  
HRSVB .A.SKVK.N.TLN.DQL.SS.K...Q.ST.DNIDTPNYDV.KHLNK...M  
BRSV .A.SKVK.N.TFN.DQL.ST.K...Q.ST.DNIDIPNYDV.KHLNK...M  
PVM ...DRLK.N.V.N.DSL.SNCK.SVT.ST.DV.S.SGHAM.KALARTL.M

100  
HMPV ILYAKHADYKYAAEIGIQYISTALGSEVQOILRNSGSEVQVVLTRTYSL  
APVC .....T..SH...V.M..V..T..A..T....K.....A...K....  
APVB ..F.....EP..QV.M.....ADKT....KS.....G.M.KIVT..  
APVA V.F...T..EP...V.M.....AD.T....K.....G.M.KIVT..  
HRSVA L.ITED.NH.FTGL..ML.AMSR..R.DTIK...DA.YH.KANGVDVTTH  
HRSVB L.ITED.NH.FTGL..ML.AMSR..R.DTIK..KDA.YH.KANGVDITTY  
BRSV L.ITED.NH.FTGL..ML.AMSR..R.DTLK..KDA.YQ.RANGVDVITH  
PVM F.LTAFNRCEEV....L..AMSL..RDDSIC...EA.YN.KC.D.QLKDF

150  
HMPV GKIKNNKGEDLOMLDINGVEKSWVEEIDKEARKTMATLLKESSGNIPQNO  
APVC ..G..S...E.....R..I..V.....SAT.DN..P....  
APVB PAEGPIR--KREV.N..DIGPA.ADNVERT..E..SLMV..K-AQ..K..  
APVA SAEGSVR--KREV.N..D.GVG.ADDVERTT.EA.GAMVR.K-VOLTK..  
HRSVA RQDI.G.EMKFEV.TLASLTTEIQIN.EI.S..SYKKM...M-EVAPEY  
HRSVB RQDI.G.EMKFEV.TLSSLTSEIQVN.EI.S..SYKKM...M-EVAPEY  
BRSV RQDV.G.EMKFEV.TLVSLTSEVQGN.EI.S..SYKKM...M-EVAPEY  
PVM TIKLQG.EYKI.V...V.IDAANLADLEIQ..GVV.KE..TG-ARL.D.R

200  
HMPV RPSAPDTPILLCVGALETPKILFSTFEVQLETFVRANRVLSDAIKRTPR  
APVC ...S..A.....I.....A.....N.....F..  
APVB K...L.A.V...I.....V.....AI...S.....IS...  
APVA K...L.A.V...I.....V.....AI...S.....IS...  
HRSVA .HDS..CGM.I..IA..VI...AGDRS..TAVI...N..KNEM...KG  
HRSVB .HDS..CGM.I..IA..VI...AGDRS..TAVI...N..KNEI...KG  
BRSV .HDS..CGM.V...A..VI...AGDRS..TAVI...N..RNEM...KG  
PVM .HD...CGV.V..IA..VVS...AGDRG..DAVE...LN..KAKA...N

250  
HMPV MDLEKIDARSEYOLEFQKVFHRSIDTFMKAIGSSSTGKAESITVNTFMC  
APVC I.....Y.....  
APVB ...R..K..FE...K...Y.N.....T.S..RM.....  
APVA ...R..K..FE...K...Y.N.....T...RM.....  
HRSVA LLPKD..N...EV..KHPHFIDV.VHF.I.QS.TRG..RV.GI.AGL..N  
HRSVB LIPKD..N...EV..KHPHLIDV.VHF.I.QS.TRG..RV.GI.AGL..N  
BRSV LIPKD..N...EV..KYPHYIDV.VHF.I.QS.TRG..RV.GI.AGL..N  
PVM .EVKQ..E.....R.P.YIDV..TF.L.QS.VRG...V.G..SGL..N

300  
HMPV AYAGGOTMERWGV FARSNNIMLGHV VQAEKROVTEVYDWHMGPESG  
APVC .....R..V.....R..S.....K.....  
APVB .....R..S.....K.....  
APVA .....V.....L.K.VK.....A...ME..V...EYAQKL.G.A.  
HRSVA .....S..V.....L.K.VK.....A...ME..V...EYAQKL.G.A.  
HRSVB .....V.....L.K.VK.....A...ME..V...EYAQKL.G.A.  
BRSV .....V.....L.K.VK.....A...ME..V...EYAQKL.G.A.  
PVM .....V.....L.K.VK.....A...ME..V...EYAOKO.G.A.

350  
HMPV DILHROS PKAGULSLANGENESVYVCA SGLGSGMYRGRVPNTLFS  
APVC .....N.....L.....A.....  
APVB .....TS.....A.....K..A..L....  
APVA .....T.....A.....K..A..L...A..  
HRSVA FY.I.LNN...S...TQF.H.S.....A...M.E...TPR.QD.YD.  
HRSVB FY.I.LNN...S...TQF...S.....A...M.E...TPR.QD.YD.  
BRSV FY.I.LNN...S...TQF...S.....A...M.E...TPR.QD.YD.  
PVM FY.I.LNN...S...T...T.....A.....S.K.APR.R...D.

395  
HMPV AESYAKSLKESNKNINFSSGLTDEEKEAAEHFLNVSDDS-QNDYE  
APVC .....R.....E.....N...INEEG-.....  
APVB .....R.....LAA...ED.R...TSY.GGDE.K-SQKF..  
APVA .....RT.R.N...LAA...D.R...TSY.GGD.ER-SSKF..  
HRSVA .KA..EQ...NGV..Y.V.D..A..L..IK.Q..PK.N--DVEL-  
HRSVB .KA..EQ...NGV..Y.V.D..A..L..IKNQ..PKE.--DVEL-  
BRSV .KA..EQ...NGV..Y.V.D..T..L..IKNQ..PK.N--DVEL-  
PVM .KD..ER..DN.V...Y.A.N..A..R.LISQQ..IV..TPDD.I-

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Fig. 9

```

HMPV MSFPEGKDILFMGNEAAKLAFAFKSLRKPCHKRS-----QSIIGEK 50
APVC .....L.....A.....R..K.I..R.T-----...V.D.
APVB ..L.....M..S.....Y.Q.IKNSTSV-----R..S.DP
APVA .....M..S.....M.D.Y.R...NTSAGG-----R..S..P
HRSVA ---M.KFAPE.H.ED.NNR.TK.LE-----
HRSVB ---M.KFAPE.H.ED.NNK.TK.LE-----
BRSV ---M.KFAPE.H.ED.NTK.TK.LE-----
PVM ---M.KFAPE.V.ED.N.K..E.L.HRSF.SE.PLAGIPNTATHVTKNM
100
HMPV VNTVSETLELPTISRPAKPTIPSEPKLAWTDKGGATKTEIKQAIVMDPI
APVC II....V.K...KST.V.T.P.R.N..GE.PDT.RSQTEE.RNEAT.E
APVB .S....KVP..PLCSSETS-----R.ACIRPT-.STLPPIK--
APVA I..IA.KVP..PLCN.TT-----..SCI.PN-.APVPKVK--
HRSVA ---IKGKFTS-----KDPKK.DS.ISVNS.
HRSVB ---IKGKFSS-----KDPKK.DS.ISVNS.
BRSV ---LKGKFTS-----KDSRK.DS.ISVNSV
PVM PPILRSSFK..SPRVA.NL.E..A.P---TTPPP.PPQN.EEQPKESDV
150
HMPV EEEESTKVKLPSSDGKTPAEKKLPSTNTKKK-----VSFTPNPEPKYT
APVC DASRLY.EVFA.T.....GKETPEKP-----T.KND.S.R..
APVB .V.SIYP.LPTAPP.AMIETAHPGAPKKAQ.R-----K.ESSKA...
APVA .I.SIYP.LPTAPVATD.YTSTTESAKKS.....K.DNPKV....
HRSVA DI.VTK.SPITSN.TIIN.TNETDDTAG.KPNYQRKPL...KEDPTPSDN
HRSVB DI.VTK.SPITSGTNIIN.TSEADSTPETKANYPRKPL...KEDLTPSDN
BRSV DI.LPK.SPITSTNQINQNPSEINDTIATNQVHIRKPL...KEEL.SSEN
PVM DI.TMHVC..PDNPEHKKPCCSDDTD.KKT---RKPM.T.VEP.EKFVG
200
HMPV KLEKDALDLSLSD-NEEEDAESSILTFEERD--TSLSIEARLESTEEKLS
APVC ...ME..E....-..DD....V.....K.-..A..L.....D...
APVB ...EE..E....PD.DN.EK..V.....K--NAPS.....A.....
APVA ...EEG.E....PE.DN.EK.....K---P.T.....A.....
HRSVA PFS.LYKETIETFDNN--E.E.SYSY..INDQ.NDN-.T...DR.D...
HRSVB PFS.LYKETIETFDNN--E.E.SYSY..INDQ.NDN-.T...DR.D...
BRSV PFTRLKETIETFDNN--E.E.SYSY..INDQ.NDN-.T...DR.D...
PVM LGASLYRETMQTFAADGYD.E.N.S...TNQEPG.S.V.O..DR.....
250
HMPV MILGLRLTLNIATAGPTAARDGIRDAMIGVREELIADIKEAKGK-----
APVC .....V.....V..L.....
APVB ...M.K..S.....V.....NS.MA.....
APVA ...M.K.....M.....NS.MT..D.....
HRSVA E...M.H..VV.S....S.....L...M.EK.RT..LMTNDRLE
HRSVB E...M.H..VV.S....S.....V.L...M.EK.RA..LMTNDRLE
BRSV E.I.M.H..VV.S....S.....V.L...M.EK.RS..LMTNDRLE
PVM Y.I...N.IMV.....T...E...L.T...EM.KSULTVNDRIV
300
HMPV -AAEMMEEEMSQRSKIGNSGVKLTEKAKELNKIVEESTSGSEDEHEHEH
APVC .....K..AK.K.....G.....
APVB -I..I.K..DA..A..D.....R...RML..Q.S...T.S.EE
APVA -I...K..DT..A..D.....L...Q.S...T.S.EE
HRSVA AM.RLRN..SEKMA.DTSDE.S.NPTSEK..NLL.G-----N
HRSVB AM.RLRN..SEKMA.DTSDE.P.NPTS.K.SDLL.....N
BRSV AM.RLRD..SEKMT.DTSDE...PTSEK..MVL.....E
PVM AMEKLRD..C.RADTDGSAKY..DR.RI.D...SSNA-----E
316
HMPV DTQDNSQEDDIYQLIM
APVC :EESNPD..L.S.T.
APVB EEDTDGEN....SFD.
APVA ESESDEEL.S...N.DL
HRSVA .SDNDLSLE.F-----
HRSVB .SDNDLSL..F-----
BRSV SSDNDLSLE.F-----
PVM EAKEDLDV...MGINF

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Fig. 10

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HMPV MESYLVDTYQGIETAAVQVDLIEKDLLPASLTIWFPLEQANTPPAVLLD 50
APVC .....V.....T.V...Q...R..V.V...T...T...E
APVB .....II....V.....V...NN..K..V...SS..AP....
APVA .....II....V.....SN..T.V...SS..AP....
HRSVA ..T.VNKLHE.ST.....YNNV...DD.....V.M..SSM.ADL.IK
HRSVB ..T.VNKLHE.ST.....YNNV...DD.....V.M..SSV.ADL.IK
BRSV ..T.VNKLHE.ST.....YNNV...DD.....V.M..SSISADL.IK
PVM ..A...EM.H.V.....LN.V..HSANI...V.I.M..TSL.KNSVM.
                                           100
HMPV QLKLTITITLYAASONGPILKVNASQGAAMSVLPKKFEVNATVALDEYS
APVC .....T.....A...S.D.S.S...D..
APVB .....S...Q.TV.PE..V.Q...T.....A...S.S.AA....
APVA .....S...Q.T...PE..V.Q...A.....A...A.S.A....
HRSVA E.ANVN.LVKQISTPK..S.R.MINSRS.VLAQM.S..TIC.N.S...R.
HRSVB E.ASIN.LVKQISTPK..S.R.TINSRS.VLAQM.SN.IIS.N.S...R.
BRSV E.INVN.LVRQISTLK..S..IMINSRS.VLAQM.S..TIS.N.S...R.
PVM L.HDV.VICTQISTVH..MI..DL.SSN.GLATM.RQ.LI..II...DWG
                                           150
HMPV KLEFDKLTVCVKTIVYLTMTKPYGMVSKFVSSAKSVGKRTHDLIACDFM
APVC .....L.A.....N...A.....L
APVB ..D.GV....D.RA....L.....I.TNMNT..R.....I
APVA R...GT....D.RSI....L.....IMTDVR..R.....I
HRSVA ..AY.VT.P..I.ACS..CL.SKN.LTTVKDLTMKTLNP...I...E.E
HRSVB ..AY.VT.P..I.ACS..CL.VKS.LTTVKDLTMKTFNP..EI...E.E
BRSV ..AY.IT.P..I.ACS..CL.VKN.LTTVKDLTMKTFNP..EI...E.E
PVM NMDYEVFVAFDK.SFCV..IL..KN.LYTVP.ITP-TNRP..E...V.S.H
                                           200
HMPV DLEKNTFVTIPAFIKSVSIKESSESATVEAAISSEADQALTOAKIAPYAGL
APVC ....GV.....Y.....G.....I...R.....
APVB ..M.RGI....Y..A...D.....G.....I...R.....
APVA ..I..GV.I....Y..A...D.....G.....I...R.....
HRSVA NIVTSKK.I..TYLR.I.VRNKDLN.L.NITTT.FKN.I.N...I..S..
HRSVB NIMTSKR.I..TYLRPI.V.NKDLNSL.NIATT.FKN.I.N...I....
BRSV NIMTSKR.V..T.LR.INV.AKDLSL.NIATT.FKN.I.N...I....
PVM NRVTLKSFN..V..RALY.RQQGLDS..Q....DV.H.I.T.RV.....
                                           250
HMPV IMIMTMNPNKGIFKKLGAGTQVIVELGAYVQAESISKICKTWSHQGTRYV
APVC .....V.....R..RN.....
APVB ..LL.A.....R.....P.....LG.....N..R...I
APVA ..L.....M.....P.....LG.....N..R...
HRSVA LLVI.VTDN..A..YIKPOS.F..D....LEK...YYVTN.K.TA..FA
HRSVB VLVI.VTDN..A..YIKPOS.F..D....LEK...YYVTN.K.TA..FS
BRSV VLVI.VTDN..A..YIKPOS.F..D....LEK...YYVTN.K.TA.KFS
PVM TLVINITST..A..L.K..S..ILA...P.LTQV.LHDVIMN.K.T..S.I
                                           258
HMPV LKSR----
APVC .....
APVB .....
APVA ..R.....
HRSVA I..PMED--
HRSVB I..PLED--
BRSV I..PIED--
PVM ...SSTSG

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Fig. 11

Signal peptide		100
HMPV	MSWKVVIIIFSLITPQHGKESYLEES	STITEGYLSVLRGTWYTNVFTLEVGDVENL
APVC	LLLV.A.TG.E	Y.V.R.
APVB	YL.LLL.IY.VVGASGKIQ.T.S	V.R.K.
APVA	DVRICLLLF.ISN.SSCIQ.T.N	V.R.K.
HRSVA	MELLILKANAITTILTAFTFCFASGONIT.EFYQST	AVSK.A.S.I.I.LSNIKENH
HRSVB	MELLILHLSAIFLTIA.NA.YL.SSONIT.EFYQST	AVSR.F.A.S.I.I.LSNIKETH
BRSV	MATTAMRMII.IIFISTYVTH.LCONIT.EFYQST	AVSR.A.S.V.I.LSKIQKNV
PVM	MIPGRIFLVLLV.NTKPIHPNT.T.K.Y.ST	VE.A.K.A.HMT.MSIKLSQINIES
Fusion domain		HRA
HMPV	LAREEQ	IENPROSRFVLGAIALGVATAAAVTAGVAIAKTIRLESEVTAIKNALKKTNEAVSTLNGVRVLATAVRELK
APVC	K.AR	MS.KA
APVB	ITK.NR	LSH.KK
APVA	V.K.SR	LSS.KR
HRSVA	PPTNNRRARELPRFMNYTLNNAKKTNTLSKK.KR	LG-FL.G-S.IAS.VS.VLH.G.NK.S.LS.K.VS.S.S.TSK.LD.
HRSVB	P.ANNRRAREAPOYMYTINTKNLNV.SKK.KR	LG-FL.G-S.IAS.I.VS.VLH.G.NK.S.LS.K.VS.S.S.TSK.LD.
BRSV	P.SFSRAKRGIPELIHYTRNSTKKFYGLMGKK.KR	LG-FL.IG-S.AS.VS.VLH.G.NK.S.LS.K.VS.S.S.TSK.LD.
PVM		ALSKK.KK.LG-LI.LG.L.VQ.IAL.RD.VRN.VS.T.MS.KV.DD.
		300
HMPV	DFVSKNLTRAINKNKDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSNMPTSAGQIKMLNENRAMVRRKGFGFLIGVYSS	
APVC	I.K.P.R.S	G.Y.V.S.N.I
APVB	E.I.K.P.Q.N	IR.I.G.N.S.S.V.VK.INR.S.S.N.I
APVA	E.I.K.P.Q.N	I.G.N.S.S.V.D.V.INR.S.S.N.I
HRSVA	NYID.Q.LPQV.QS.S.SNIETVIE.Q.K.N.L.EIT.E.V.V.TFV.TYML.NS.LSLIND.ITND.K.SN.VQI.QQSYSIMSIIKEEV	
HRSVB	NYINNO.LPQV.QQS.R.SNIETVIE.Q.K.S.L.EIN.E.V.V.TPL.TYML.NS.LSLIND.ITND.K.SS.VQI.QQSYSIMSIIKEEV	
BRSV	NYID.E.LPQV.NHD.R.SNIETVIE.Q.K.N.L.EIA.E.V.V.TPL.TYML.NS.LSLIND.ITND.K.SS.VQI.QQSYSIMSIIKEEV	
PVM	N.I.E.LPK.RVS.VH.ITAVIR.Q.L.K.L.E.S.E.S.L.HTV.SFML.R.TSI.GG.AV.KEI.SSK.IM.N.LAI.SS.NADT	
		400
HMPV	VIYMVQLPIFGVIDTHIVKAAPSQSG--KKGNYAQLLREDQGWQONAGSTVYYPNEKICETRGDHVCOTAAAGINVAEQSKHCININISTTNYICKVS	
APVC	V.I	K.D.E.V.S.E.R.K
APVB	V	E.R.V.LRH--ERES.T.A.D.V.D.Y.SEVEG.H.ST
APVA	V	E.R.V.LRK--E.T.A.KD.V.D.Y.LEVEG.Y.SK
HRSVA	LA.V.LY	KLHTS.I.TTNT.E.SNI.T.T.R.D.VSFF.QAET.KVQSNR.MNSLTLPSEINI.VD.FNPK.I.IM
HRSVB	LA.V.Y	KLHTS.I.TTNI.E.SNI.T.T.R.D.VSFF.QAET.KVQSNR.MNSLTLPSEVSI.TD.FNSK.I.IM
BRSV	IA.V.Y	KLHTS.I.TTDN.E.SNI.T.T.R.D.VSFF.QTET.KVQSNR.MNSLTLPDVTI.TD.FN.K.I.IM
PVM	LV.VI.L.M	L.VIRSSIIHN--IADK.A.A.N.H.LS.F.SPT.IHNGYA.LKSLT.PVT.R.S.MY.D.I
		500
HMPV	TGRHPISMVALSPGLALVPCYKGVSCBIGSNRVGIIKQLNKGCBIYTNOQADTVIDNTVYQLSKVEGEQHVIGRVPSSSFDPVKFPEDQENVALDOVF	
APVC		D.M.K.RP.G.S.T.K.N.IE.I
APVB	V	T.G.S.E.K.TH.P.NE.I.I.V.RT.A.VNN.N.LL
APVA	V	T.G.S.E.S.K.TH.P.NE.I.I.V.RT.A.VNN.N.LL
HRSVA	SKTDV.SSVITS.I.S	GKTK.TASNKNR.TFSN.D.VS.KGM.SVG.L.YVN.Q.KSLYV.E.IIFY.LV.S.E.DASIS.N
HRSVB	SKTD.SSVITS.I.S	GKTK.TASNKNR.TFSN.D.VS.KGV.SVG.L.YVN.L.KNLYV.E.IIFY.LV.S.E.DASIS.N
BRSV	SKTD.SSVITS.I.S	GKTK.TASNKNR.TFSN.D.VS.KGV.SVG.L.YVN.L.KALY.E.IIFY.LV.S.E.DASIS.N
PVM	SKTYV.TAV.TTH.C.S	GHN.FVIN.DK.RT.PD.S.KGV.R.QVG.Y.EV.KSI.VR.E.LVLKY.LS.D.K.D.IRD.E
HRB		583
HMPV	ESIENSQALVDQSNRILSSAE--KGNTGFIIVIIILAVLGSTMLVSVFIIKKTKKPTG--AP-PELSGVTNNGFIPHN	
APVC	V.K.N.I.K.D.I	A.V.V.VL.MLAARG.G.FVV.R.AAPK--F.M.MN.N.K
APVB	VDK.KD.I.K.DL.DIEV--S.I.AALA.TILV.SMLI.VGLAYYVV.R.AK.S--NGY.KTT.QS.M.Y.S--	
APVA	DR.D.I.K.DL.GADA--SKA.IA.A.VVLVI.IFFL.AVIYYCSRVR.TKPK--HDY.ATT.HSSMAYVS--	
HRSVA	K.NO.L.FIRK.DEL.HNVN--AG.ST.NIM.TT.I.VIIIVILLS.IA.GLLLYCKARS.P-VTLKSDQ..IN.IA.SN--	
HRSVB	K.NO.L.FIRR.DEL.HNVN--TG.ST.NIM.TT.I.VIIIVILLS.IA.GLLLYCKA.N.P-VTLKSDQ..IN.IA.SK--	
BRSV	AK.NO.L.FIRR.DEL.H.VD--VG.ST.NVV.TT.I.VIIIVILLS.IA.GLLFYCKT.S.P-IMLCKDQ..IN.LS.SK--	
PVM	H.NOTRTFFKA.DQL.DLS.NREN.NLNKSY.LTT.LE.VMLII.MAVIGF.LY.VL.MIRDNKLKSKSTP.L.VLS--	

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Fig. 12

A

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# # # 50
HMPV MSRKAPCKMWRCKCNRGSECKENHNYSWPDRLRSNYILNQLRNW
APVC .....L.....
APVB ..GRN..R..T..R.....S.T.....HV..V.A..M...V...
APVA ...RN..R..I.....S.T.....HV..V.A..M.....
HRSVA ...RN...F.I..H.LN.KR.H.S...FE..PHA..V.Q.FM..RI.KSM
HRSVB ...RN...F.I..H.LN.RR.HYS...FE..PHA..V.Q.FM..KI.KSM
BRSV ...RN.....I..H.LN.KK.H.S...FE..PHA..V.Q.FM..KI.KSM
PVM ...VR...F..Q.F.S..RN..YS.K..E..LKT.ML.Q..M..RIY.FL

# 100
HMPV DRADGLSITISEAGREDRTQDFVLGSTNVQGYIDDNQSITKAAACYS LH
APVC ..S.....L.....D.....N...N.EN...ST....Y
APVB ..T.....L.....A...N..EG.AT...S.....Y
APVA ..T.....L.....A...N..EG.TT...S.....Y
HRSVA .KSI.T..E...AEL...EEYA..VVG.LES..GSINN...QS..VAMS
HRSVB .KSI.T..E...AEL...EEYA..IVG.LES..GSINN...QS..VAMS
BRSV ..NN.T..E...AEL...EEYA..VIG.LES.LGSINN...QS..VAMS
PVM .TNT.AI.DV..FDAPQ..AEYA..TIG.LKS.LEKTNN...SI..G..I

150
HMPV NIIKQLQEVEVRQARDNKLSDSKHVALHNLVLSYMEMS-KTPASLINNLK
APVC .....TD.....VD.....
APVB .....ND.KS...LMVD.P.....ID...N..N...S..
APVA .....ND.KTS..SM.E.P.....I...VD...N.....S..
HRSVA KLLTE.NSDDIKKL...EELN.PKIRVY.T.I..I.SNR.NNKQT.HL..
HRSVB KLLTEINSDDIKKL...EELN.PKIRVY.T.I..I.SNR.NNKQT.HL..
BRSV KLLAEINNDIKRL.NKEVPT.PKIRIY.T.I..IDSNKRTKQT.HL..
PVM TVLQN.DVGL.I....SNTE.TNYLRSC.TI...IDKIL.K-RQI.HI..

195
HMPV RLPREKLKKLAKLIIDLSAGAE--NDSSYALQDSESTNOVQ----
APVC K..K.....E...V---TA.M...ANS-----
APVB ...K.....I..Q...S.GE.AN.NT..KGD.S.-----
APVA .....I..Q...P.SD.A.GNT..KGD.N.-----
HRSVA ...ADV...TI.NTL.IHKSITIN.PKESTVS.TNDHAKNNDTT-
HRSVB ...ADV...TI.NTL.IHKSIIIS.PKESTVN.QNDQTKNNDITG
BRSV ...ADV...TI.NT..IHNEINGN.QGDIIIVNEQNE-----
PVM ...VGV.CN.IQSV.SIEEKINSSMKTE-----

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B

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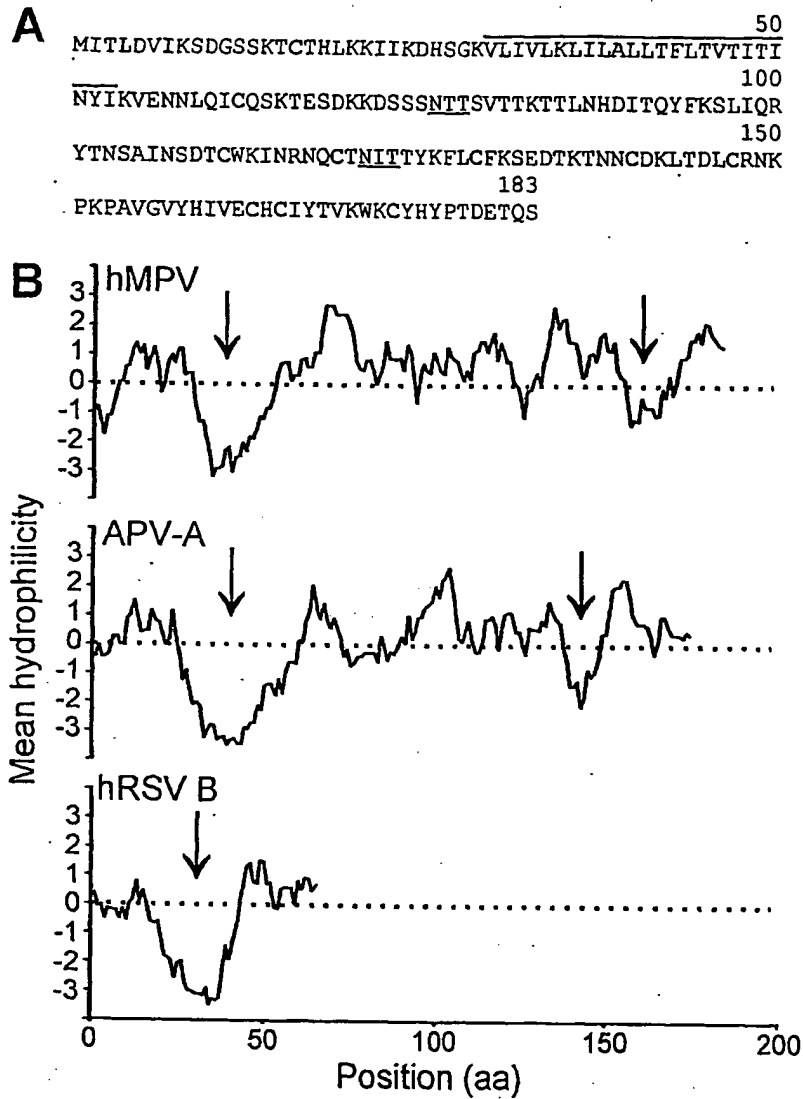
# 50
HMPV -----MTLHMP-CKTVKALIKCS-----EHGPFVETIEVDDMIW
APVC -----...QL...I.QT....G-----LI.LKMKL...V.
APVB -----PIVI...R.T.V.R.N-----TL.VCLFKRTYEHN.I
APVA -----PVVI...RR.T.I...N-----AL.LCMVRKTY.YS.A
HRSVA MTMPKIMILPDKY.-.SITSI..TSRCRVTMYNQKNTLY.NQNNPNNHMY
HRSVB MTKPKIMILPDKY.-.SISSI..SSESMIATFNHKNILQ.NHNHL.NHQR
BRSV MNNSNIIIFPEKY.-.SISSL...NENDVIVLSHQNVLDYLFQYPCNMY
PVM MQSDPICHHRGEDKFFYENRM.RLPKYYPAILHKMYIIRVNRNLTIDGS

97
HMPV THKDLKEA---L---SDGIVKSHNTNIYNCYLENIEIIVKAYLS---
APVC .KNE.VDI---I---TE...V.A..FK.R..D.....TF.-----
APVB NLG..I.E---V---ARM.IID.I.RKQ.NECKRDFEF.AV.T.YT--
APVA SWS..I.E---V---ANMVLID.I.RKQ.VECRKDFEF.TI.YN--
HRSVA SPNQTFENE---IHWT.QELIDTIQ.FLQHLGIED.YTIYILV.----
HRSVB LLNNIFDE---IHWT.PKNLLDATQQFLQHLNIPED.YTIYILV.----
BRSV SQNHMLDD---IYWT.QELIEDVLK.LHLSGIS.SKYVIYVLV----
PVM GPSTIID.GKSVVWNRVDVIACVKEALC.IEFSWNNQVIIDFDYSQAR

```

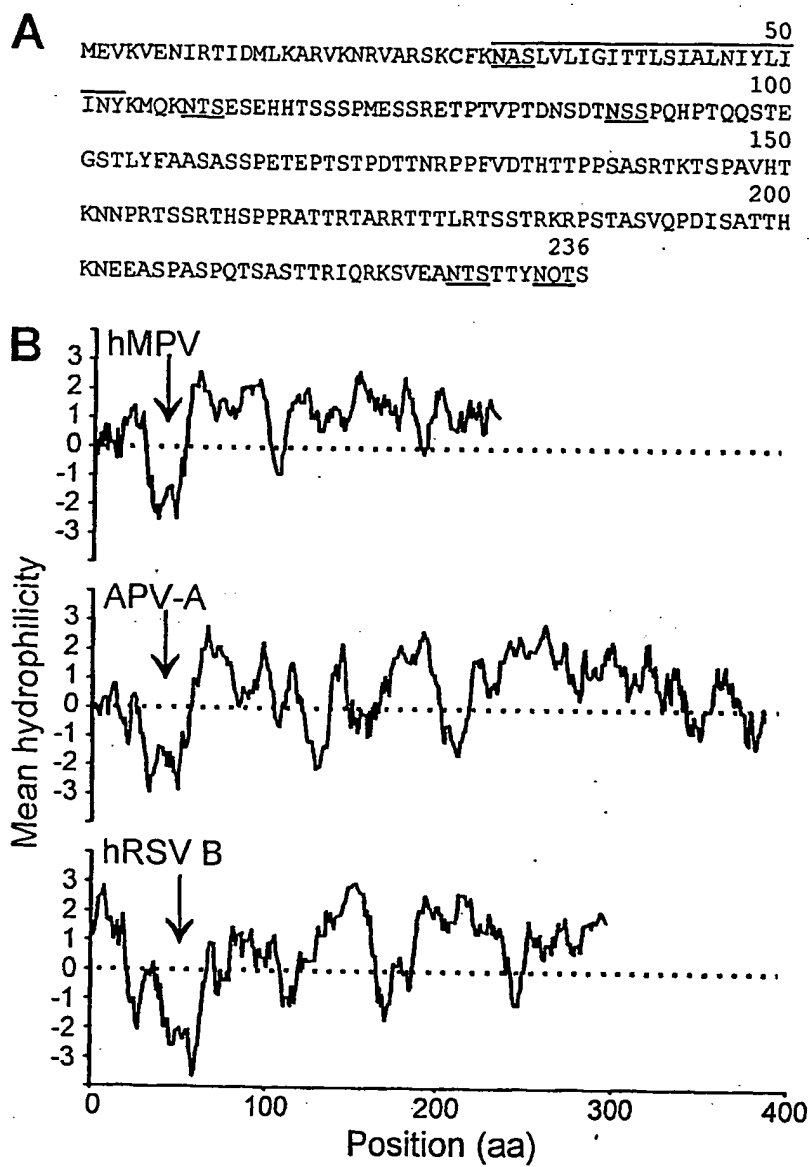
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Fig. 13



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Fig. 14



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Fig. 15

**A**

674

HMPV NYIARASIVTDLSEFNQAERYETTAICADVADLHGTQSLFCWLHLIVPM  
 APVA .....SV.....T.SS  
 HRSVA ...SKQ...I.....SC..S..L....V...F...AI.H  
 HRSVB ...SKQ...I.....SC..S..L....V...S...TI.L  
 BRSV ...SKQ...I.....SC..S..L....V...S...TI.F  
 HPIV2 FELSACF.T...A.YCLOW..Q.IIHF.RTLNRMV.VPH..E.I..RLIR  
 NDV RRRVATF.T...Q.YCLNW..Q.IKLF.HAINQ.M.LPHE.E.I..RLMD  
 SV YETLSQFLT...K.YCLNW..F.S..LFGQRCN.IF.FKTF.N.M.PVLEK  
 HPIV3 YETVSCFLT...K.YCLNW..S..LFGTCNQIF.LNK..N...PRLEG  
 MV YETVS.F.T...K.YCLNW..S..LFGTCNQIF.LNK..N...PRLEG  
 NIPAH FDTVS.FLT...K..CLNW...SM..F.ERL..IY.LPGF.N.M.KRLER

**B**

723

HMPV TTMICAYRHAPPETKG-EYDIDKIEEQSGLYRYHMGGIEGWCKLWTMEA  
 APVA .....D.G.-I.....Q.P.....F.....M.....  
 HRSVA V.I..T.....YIRDHIV.LNNVD.....I..  
 HRSVB V.I..T.....FI.DHVNLNEVD.....I..  
 BRSV A.V..T.....YIRNHIT.LN.VD.....I..  
 HPIV2 S.LYVGDPFN..AATD-AF.L..VLNGIIFIVSK.....L..M...IS  
 NDV ...FVGDPFN..SDPT-DC.LSRVPNDIYIVSAR.....L.....IS  
 SV C.IYVGDPYC.VADRM-HRQLQDHADSGIFIHNP.....Y.....LIS  
 HPIV3 S.IYVGDPYC..SD.E-HISLEDPDSCFYVHNPR.....F.....LIS  
 MV SVLYVSDP.C..DLDA-HIPLY.VPNDQIFIK.P.....Y.....IST  
 NIPAH SVIYV.DPNC..NIDK-HMELE.TP.DQIFIH.PK.....YS..T..IAT

**C**

772

HMPV ISLLDVSVKTRCMTISLLNGDNQSDVSKPKVLESEG-LDEVKADYSLAV  
 APVA .....RN.V.L.....R.TGA-QT.IQ.....I  
 HRSVA ...LI..L.GKFSI..A.I.....I...R.M..-QTHAQ...L..L  
 HRSVB ...LI..L.GKFSI..A.I.....I...R.I..-QTHAQ...L..L  
 BRSV ...LI..L.GKFSI..A.I.....I...I..N..-QTHAQ...L..L  
 HPIV2 ..VILLS.AESKTRVM..MVQ...A.A.TTR.PR.LPSIQKKELA.AASK  
 NDV ..AAQLAAARSH.RVPCMVQ...V.A.TRE.RSDDSPENVLTQLHOASD  
 SV ..AIHLAA.RVGVRSAMVQ...A.A.TSR.PVAQTYKQKKNHV.EEIT  
 HPIV3 ..AIHLAA.RIGVRV..AMVQ...A.A.TTR.PNNYDYRIKKEIV.KDV.  
 MV ..PY..YLAAYESGVRI..VQ...T.A.T.R.PSTWPYNLKKREARVTR  
 NIPAH ..PF..FLSAYE.NTRIPAIVO...E..AITQK.HPNLPYKKEICAKQ.Q

**D**

822

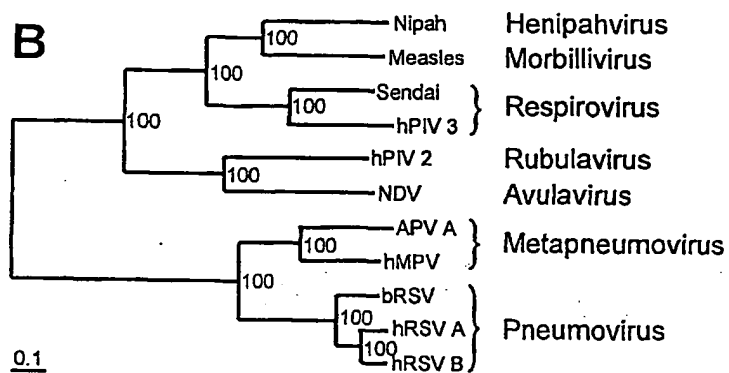
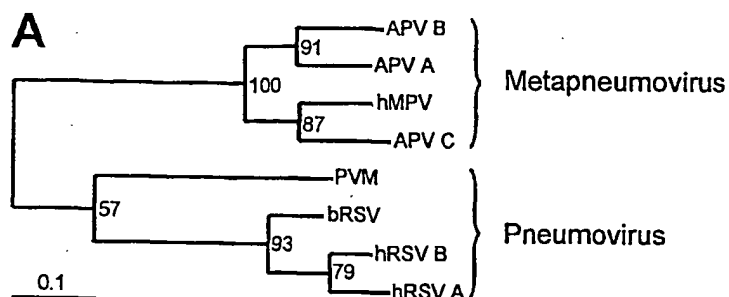
HMPV KMLKEIRDAYRNIGHKLKEGETYISRDLOFISKVIOSEGVMHPTPIKKIL  
 APVA ...TAV...Y.....V.....M..T.....Y.AA...V.  
 HRSVA NS..LLYKE.AG.....GT.....M..M..T..HN..YY.AS...V.  
 HRSVB NS..LLYKE.AG.....GT.....M..M..T..HN..YY.AS...V.  
 BRSV ..S..LLYKE.AS.....GT.....M..M..T..HN..YY.AS...V.  
 HPIV2 LFFERL.ANNYGL..Q..AQ..I..STFFIY..RVFYQ.RILQAL.NAS  
 NDV NFF..LIHVNL..N..DR..IR.DTFFIY..R.FKD.AILSQVL.NSS  
 SV RYFGAL.HVMFD...E..LN..I..SKMFVY..R.YYD.KIL.QCL.AIT  
 HPIV3 RFFDSL.EVMDL..E..LN..I..SKMFVY..R.YYD.RIL.QAL.AIS  
 MV DYFVIL.QRLHD...H..AN..IV.SHEFFVY..G.YYD.LLVQSLS.S.A  
 NIPAH LYFERL.MNL.AL..N..AT..I..TH.FIY..K..HYD.AVLQAL.SMS

847

HMPV RVGFWINTILDDIKTSAESIGSLCQ  
 APVA .....M.A.....  
 HRSVA .....F.V.L.....T.  
 HRSVB .....F.V.L.....T.  
 BRSV .....F.V.M.....T.  
 HPIV2 KLCLTADVLGECTQA.CSNSATTIM  
 NDV KLVLVSGDLSENTVM.CAN.A.TVA  
 SV .CVF.SE.LV.ENRSACSN.STSIA  
 HPIV3 .CVF.SE.VI.ETRSASSNLATSEA  
 MV .CVF.SE..V.ETRAACSN.ATTMA  
 NIPAH .CCF.SE.LV.ETRSACSN.STTIA

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Fig. 16



[illegible]

hMPV Le: 3' UGCUCUUUUUUUGCGCAUAUUAUAAUCUAAAGGUUUUUUUUAUACCCU  
|||||  
hMPV Tr: 5' ACGAGAAAAAAC CGUAUACAUCCAAUAUAUAUUAUUCUUAUUUU  
|||||  
  
hMPV Tr: 5' ACGAGAAAAAACCGUAUACAUCCAAUAUAUAUUAUUCUUAUUUUUA  
|||||  
APV Tr: 5' ACGAGAAAAAACCGUAUUAUCAUAUAUUUUUAAGCUUUUAAGUUUUU  
|||||  
  
hMPV Le: 3' UGCUCUUUUUUUGCGCAUAUUAUUAUAAAGGUUUUUUUUAU-ACCC  
|||||  
APV Le: 3' UGCUCUUUUUUUGCGUA-AGUUCGCGCAGAUUUUUUAUUAACCC

Fig. 17

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Fig. 18a

Comparison of two prototypic hMPV isolates with APV-A and APV-CDNA similarity matrices

<u>N</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,862	0,757	0,660
99-1	---	1,000	0,757	0,663
APVC	---	---	1,000	0,656
APVA	---	---	---	1,000

<u>P</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,811	0,677	0,588
99-1	---	1,000	0,674	0,593
APVC	---	---	1,000	0,584
APVA	---	---	---	1,000

<u>M</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,865	0,766	0,695
99-1	---	1,000	0,773	0,707
APVC	---	---	1,000	0,705
APVA	---	---	---	1,000

<u>F</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,838	0,706	0,662
99-1	---	1,000	0,716	0,655
APVC	---	---	1,000	0,685
APVA	---	---	---	1,000

<u>M2-1</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,863	0,764	0,668
99-1	---	1,000	0,744	0,657
APVC	---	---	1,000	0,670
APVA	---	---	---	1,000

<u>M2-2</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,861	0,648	0,486
99-1	---	1,000	0,675	0,486
APVC	---	---	1,000	0,463
APVA	---	---	---	1,000

<u>SH</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,688	N.A.	0,421
99-1	---	1,000	N.A.	0,380
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

<u>G</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,543	N.A.	0,262
99-1	---	1,000	N.A.	0,263
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000



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Fig. 18b

<u>5'L</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,835	N.A.	0,596
99-1	---	1,000	N.A.	0,605
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L: only the first 1500 nucleotides of 99-1 were available.  
N.A.: sequence not available.

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Protein similarity matrices

<u>N</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,949	0,880	0,685
99-1	---	1,000	0,883	0,682
APVC	---	---	1,000	0,700
APVA	---	---	---	1,000

Fig. 19

<u>P</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,860	0,683	0,552
99-1	---	1,000	0,676	0,549
APVC	---	---	1,000	0,528
APVA	---	---	---	1,000

<u>M</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,976	0,874	0,775
99-1	---	1,000	0,874	0,763
APVC	---	---	1,000	0,775
APVA	---	---	---	1,000

<u>F</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,938	0,810	0,677
99-1	---	1,000	0,803	0,674
APVC	---	---	1,000	0,719
APVA	---	---	---	1,000

<u>M2-1</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,946	0,844	0,719
99-1	---	1,000	0,834	0,703
APVC	---	---	1,000	0,704
APVA	---	---	---	1,000

<u>M2-2</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,901	0,563	0,246
99-1	---	1,000	0,577	0,232
APVC	---	---	1,000	0,191
APVA	---	---	---	1,000

<u>SH</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,570	N.A.	0,178
99-1	---	1,000	N.A.	0,162
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

<u>G</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,326	N.A.	0,094
99-1	---	1,000	N.A.	0,107
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

<u>5'L</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,921	N.A.	0,600
99-1	---	1,000	N.A.	0,594
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L: only the first 500 amino acid residues of 99-1 were available.

N.A.: sequence not available.

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Fig.20

Amino acid sequence alignment of two prototype hMPV isolatesNucleoprotein (N)

	10	20	30	40	50	60
00-1	MSLQGIHLS	DL SYKHAILKESQYTI	KRDVGT	TTAVTPSS	LQQEITLL	CGEILYAKHADYK 60
99-1	MSLQGIHLS	DL SYKHAILKESQYTI	KRDVGT	TTAVTPSS	LQQEITLL	CGEILYTKHTDYK 60
	70	80	90	100	110	120
00-1	YAAEIGIQYI	STALGSERVQQILRNSG	SEVQVVLTR	TYSLGKIKNNK	GEDLQMLDI	HGVE 120
99-1	YAAEIGIQYI	CTALGSERVQQILRNSG	SEVQVVLTK	TYSLGKCKNSK	GEELOMLDI	HGVE 120
	130	140	150	160	170	180
00-1	KSWVEEIDKEARKTM	ATLLKESSGNIPQ	NQRPSAPD	TPILL	CVGALIFT	KLASTIEVGL 180
99-1	KSWIEEIDKEARKTM	ATLLKESSGNIPQ	NQRPSAPD	TPILL	CVGALIFT	KLASTIEVGL 180
	190	200	210	220	230	240
00-1	ETTVRRANRVL	SDALKRYPRMDIP	KIARSFYDL	FEQKVYHRS	LFIEYGKAL	GSSSTGSKA 240
99-1	ETTVRRANRVL	SDALKRYPRIDIP	KIARSFYEL	FEQKVYYRS	LFIEYGKAL	GSSSTGSKA 240
	250	260	270	280	290	300
00-1	ESL FVNIFMQAYGAGQ	TMLRWGV	IARSSNNIM	LGHVSVQAE	LKQVTEV	YDLVREMGPESG 300
99-1	ESL FVNIFMQAYGAGQ	TLLRWGV	IARSSNNIM	LGHVSVQSE	LKQVTEV	YDLVREMGPESG 300
	310	320	330	340	350	360
00-1	LLHLRQSPKAGLL	SLANCPNFASV	VLGNASGL	GIIGMYRGR	VPNT	ELFSAAESYAKSLKE 360
99-1	LLHLRQSPKAGLL	SLANCPNFASV	VLGNASGL	GIIGMYRGR	VPNT	ELFSAAESYARSLKE 360
	370	380	390			
00-1	SNKINFSSLGLTDEE	KEAAEHFLNVS	DSQNDYE			394
99-1	SNKINFSSLGLTDEE	KEAAEHFLNMS	QDNQDDYE			394

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Fig.21

Phosphoprotein (P)

	10	20	30	40	50	60	
00-1	MSFPEGKDILFMGNEAAKLA	FAFQKSLRKP	GHKRSQSI	IGKVN	TVSETLE	LPTISRPAK	60
99-1	MSFPEGKDILFMGNEAAKIA	FAFQKSLKKS	GHKRTQ	SIVGEK	VNTISETLE	LPTISKPAR	60
	70	80	90	100	110	120	
00-1	PTIPSEPKLAWTDKGGATK	TEIKCATK	VMDPI	EEEEEST	TEKKVLPSSD	GKTPAEKKLK	EST 120
99-1	SSTILLEPKLAWADNSG	ITKITEKPA	KTTPV	EEEEEF	NEKKVLPSSD	GKTPAEKKSK	EST 120
	130	140	150	160	170	180	
00-1	NTKKKVSFT	NEPGKYTKLEKD	ALDLS	DNEEE	DAESSILT	FEERDTSSLSIEARLESIE	180
99-1	SVKKKVSFT	NEPGKYTKLEKD	ALDLS	DNEEE	DAESSILT	FEKDTSSLSIEARLESIE	180
	190	200	210	220	230	240	
00-1	EKL	SMILG	LLRTLNI	ATAGPTA	ARDGIR	DAMIGVREELIADI	IIKEAKGKAAEMMEEEMSQ 240
99-1	EKL	SMILG	LLRTLNI	ATAGPTA	ARDGIR	DAMIGIREELIAEII	KEAKGKAAEMMEEEMNQ 240
	250	260	270	280	290		
00-1	RSKIGN	SVKLT	EKAKELN	KIVEDE	STSGE	SEEEEEPKDTQDNSQ	EDDIYQLIM 294
99-1	RSKIGN	SVKLT	EKAKELN	KIVEDE	STSGE	SEEEEEPKETQDNNQ	GEDIYQLIM 294

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Fig.22

Matrix protein (M)

	10	20	30	40	50	60						
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	MESYLVD	TYQGIP	YTAAVQ	VDLIEK	DLLPAS	LTIWFP	LFQANT	PPAVLL	DQLKTL	TITL	60
99-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	MESYLVD	TYQGIP	YTAAVQ	VDLVEK	DLLPAS	LTIWFP	LFQANT	PPAVLL	DQLKTL	TITL	60

	70	80	90	100	110	120						
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	YAASQNG	PILKVN	ASAQGA	AMSVLP	KKFEVN	NATVAL	DEYSKL	EFDKLT	VCVKT	VYLT	120
99-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	YAASQNG	PILKVN	ASAQGA	AMSVLP	KKFEVN	NATVAL	DEYSKL	DFDKLT	VCVKT	VYLT	120

	130	140	150	160	170	180						
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	KPYGMV	SKFVSS	AKSVGK	KTHDLI	ALCDFM	DLKNI	IPVTIP	AFIKSV	SIKESE	SATVEA	180
99-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	KPYGMV	SKFVSS	AKSVGK	KTHDLI	ALCDFM	DLKNI	IPVTIP	AFIKSV	SIKESE	SATVEA	180

	190	200	210	220	230	240							
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ISSEAD	QALTQ	AKIAPY	AGLIM	MTMNN	PKGIF	KKLGAG	TQVIV	ELGAYV	QAESIS	KICK	240
99-1	..... ..... ..... ..... ..... ..... ..... ..... ..... .....	ISSEAD	QALTQ	AKIAPY	AGLIM	MTMNN	PKGIF	KKLGAG	TQVIV	ELGAYV	QAESIS	SRICK	240

	250				
00-1	..... ..... .....	TWSHQG	TRYVL	KSR	254
99-1	..... ..... .....	SWSHQG	TRYVL	KSR	254

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Fig.23

Fusion protein (F)

	10	20	30	40	50	60	
00-1	MSWKVVII	FSLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC	60				
99-1	MSWKVMII	FSLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC	60				
	70	80	90	100	110	120	
00-1	ADGPSLIKTELDLT	TKSALRELRTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA	120				
99-1	TDGPSLIKTELDLT	TKSALRELKTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA	120				
	130	140	150	160	170	180	
00-1	GVAIAKTIRLESEV	TAIKNA	LKKTNEAVSTLGN	GVRLATAVRELKDFVSKNLT	RAINKN	180	
99-1	GIAIAKTIRLESEV	NAIKG	ALKQTNEAVSTLGN	GVRLATAVRELKEFVSKNLT	SAINRN	180	
	190	200	210	220	230	240	
00-1	KCDIADLKM	AVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSNMPTSAGQ	240				
99-1	KCDIADLKM	AVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSYMPTSAGQ	240				
	250	260	270	280	290	300	
00-1	IKLMLENRAMVRRK	GFGLIGVYGSSVIYMQLP	IFGV	IDTPCWIVKAAPSCSCKK	GNYA	300	
99-1	IKLMLENRAMVRRK	GFGLIGVYGSSVIYMQLP	IFGV	IDTPCWIIKAAPSCSEK	GNYA	300	
	310	320	330	340	350	360	
00-1	CLLREDQGWY	CQNAGSTVYYPNEKDCETRGDHFCDTAAGINVAEQSKECNINISTTNYP	360				
99-1	CLLREDQGWY	CQNAGSTVYYPNEKDCETRGDHFCDTAAGINVAEQSRECNINISTTNYP	360				
	370	380	390	400	410	420	
00-1	CKVSTGRHPISM	VALSPLGALVACYKGVSCSIGSN	EVGIIKQLNKGCSYITNQDADTVTI	420			
99-1	CKVSTGRHPISM	VALSPLGALVACYKGVSCSIGSN	EVGIIKQLNKGCSYITNQDADTVTI	420			
	430	440	450	460	470	480	
00-1	DNTVYQLSKVEGE	QHVIGRPVSSSFDPVKFPEDQFNVALDQVFESIENSQALVDQSNRI	480				
99-1	DNTVYQLSKVEGE	QHVIGRPVSSSFDPIKFPEDQFNVALDQVFESIENSQALVDQSNKI	480				
	490	500	510	520	530		
00-1	LSSAEKGNTGFI	IVIIILVAVLGS	TMIIVSVFIIIIKKT	KKPTGAPPELSGVTNNGFIPHN	539		
99-1	LNSAEKGNTGFI	IVVILVAVLGS	TMIIVSVIIIIKKT	TRKPTGAPPELNGVTNNGFIPHS	539		

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Fig.24

22K protein (M2-1)

	10	20	30	40	50	60	
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	MSRKAPCKYEVRGKCNRGSECKFNHNYWSWPDYLLIRSNYLLNQLLRNTDRADGLSIIS	60				
99-1	MSRKAPCKYEVRGKCNRGSDCKFNHNYWSWPDYLLLRSNYLLNQLLRNTDKADGLSIIS	60					
	70	80	90	100	110	120	
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	GAGREDRTQDFVLGSTNVVQGYIDDNOSITKAAACYSLHNI IKQLQETEVVRQARDNKLSD	120				
99-1	GAGREDRTQDFVLGSTNVVQGYIDDNOCITKAAACYSLHNI IKQLQETEVVRQARDNKLSD	120					
	130	140	150	160	170	180	
00-1	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....	SKHVALHNLVLSYEMSKTPASLINNLKRLPREKLKKLAKLIIDLSAGAENDSSYALQDS	180				
99-1	SKHVALHNLILSYEMSKTPASLINNLKRLPREKLKKLARLIIDLSAGTDNDSSYALQDS	180					
	..... ...						
00-1	ESTNQVQ	187					
99-1	ESTNQVQ	187					

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Fig.25

M2-2 protein (M2-2)

	10	20	30	40	50	60
	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....					
00-1	MTLHMPCKTVKALIKCSEHG	PV	FFITIE	VDDMIWTHKDLKE	ALSDGIVKSHTNIY	NCYLEN 60
99-1	MTLHMPCKTVKALIKCSKHG	PK	FFITIE	ADDMIWTHKELKE	TLSDGIVKSHTNIY	SCYLEN 60

	70
	..... ..... .
00-1	IEIIYVKAYLS 71
99-1	IEIIYVKTYLS 71



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Fig.26

Short hydrophobic protein (SH)

	10	20	30	40	50	60	
00-1	MITLDVIKSDGSSKTC	HLKKIIK	DHSGKVLIVLKLILALLTF	LT	VITITINYIKVENNLQ	60	
99-1	MKTLDVIKSDGSSETC	NQLKKIIK	DHSGKVLIALKLILALLTF	FT	TATITVNYIKVENNLQ	60	

	70	80	90	100	110	120	
00-1	ICQSKTESDKKDSS	NNTTSVTTKTT	LNHDITQYEKSLI	QRYTNSAIN	SDTCWKINRNQC	119	
99-1	ACQPKNESDKKVT	KPNNTTSITT	IRETEDEPTVVH	LKRLIQRHTNS	VTKDS	SDTCWRIHKNQR	120

	130	140	150	160	170	180	
00-1	TNITTYKFLCFK	SEDTKTNNCDKLT	DLCRNKPKPAV	GVYHIVECHCIYT	VKWKC	YHYPTD	179
99-1	TNIKIYKFLCSG	FTNSKGTDC	EEPTALCDK	KLKTIVEKHK	AECHCLHTTE	WGCLHP---	177

00-1	ETQS	183	
99-1	----	177	

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Fig.27

Attachment glycoprotein (G)

	10	20	30	40	50	60	
00-1	MEVKVENIR	ITIDM	KARVKNRV	ARSKCFKNAS	LVIGIT	TL	SIALNIYLIINYKMQKNTS 60
99-1	MEVRVENIR	ITIDM	KAKIKNRI	RSSRCYRNAT	LILIGLT	AL	SMALNIFLIIDHATLRNMI 60
	70	80	90	100	110	120	
00-1	ESEHHT	SSSPME	SSRETP	TVPTD	NSDTN	SSPOHPTQ	OSTEGSTLYFAASASSPETEPTST 120
99-1	KTEN	CANMPSAE	PSKKT	PM	STAGPNT	KPNPQ	QATOWTTENSTSPVATPEGHPYTGTTQT 120
	130	140	150	160	170	180	
00-1	EDTTNR	PPFVD	TH	TPPSAS	R	TKTS	PAVHTKNNPRTSSRTHSPPRATTTRTARRTTTLRTS 180
99-1	SDTTA	PQQT	TDKHTA	PLKST	NEOIT	TOTTTEKKTIRATTO	KREKGKENTNOTTSTAATOTT 180
	190	200	210	220	230		
00-1	STRKR	PSTAS	VQPD	ISAT	THKNEE	ASPASPQTS	ASTTRIQRKSVEANTSTTYNQTS 236
99-1	NTTNQ	IRNASE	T-----	ITTS	DRPRT	DTTITQSSE	QTTRATDESSPPHHA----- 224

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Fig.28

N-terminus of polymerase protein (L)

	10	20	30	40	50	60	
00-1	MDP	IN	ESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVIEHVRL	60			
99-1	MDP	EC	ESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVVEHVRL	60			
	70	80	90	100	110	120	
00-1	KNAV	NSKMKISDYKIVEPVNMQHEIMKNVHSC	ELTLLKQFLTRSKNISTLKLNMICDWLQ	120			
99-1	RNAV	MTKMKISDYKVVEPVNMQHEIMKNIHSC	ELTLLKQFLTRSKNISSLKLNMICDWLQ	120			
	130	140	150	160	170	180	
00-1	LKSTSD	DTSILSFIDVEFIP	SWVSNWFSNWNLNKLILEFRKEEVIRTGSILCRSLGKLV	180			
99-1	LKSTSD	NTSILNFIDVEFIP	VWVSNWFSNWNLNKLILEFRREEVIRTGSILCRSLGKLV	180			
	190	200	210	220	230	240	
00-1	FVVSSYG	CIVKSNKSKRVSFFT	YNQLLTWKDVMLSRFNANFCIWVSNL	NENQEGGLRS	240		
99-1	FIVSSYG	CVVKS	NKSKRVSFFT	YNQLLTWKDVMLSRFNANFCIWVSNL	NKNQEGGLRS	240	
	250	260	270	280	290	300	
00-1	NLQG	ILTNKLYETVDYMLSLCCNEGFS	LVKEFEGFIMSEILRITEHAQFSTRFRNTLLNG	300			
99-1	NLQG	MLTNKLYETVDYMLSLCCNEGFS	LVKEFEGFIMSEILKITEHAQFSTRFRNTLLNG	300			
	310	320	330	340	350	360	
00-1	LTDQ	LTKLKNK	NRLRVHGT	VLENNDYPMEVVLKLLGDTLRC	IKLLINKNL	ENAAELYI	360
99-1	LTEQ	LSVLKAK	NRSRVLGT	ILENNNYPMEVVLKLLGDTLKS	IKLLINKNL	ENAAELYI	360
	370	380	390	400	410	420	
00-1	FRIF	GHMPVDERDAMDAVKLNNEITKILR	WESLTEL	RGAFILRIIKGFVDNNKRWPKIKN	420		
99-1	FRIF	GHMPVDEREAMDAVKLNNEITKILK	LES	TEL	RGAFILRIIKGFVDNNKRWPKIKN	420	
	430	440	450	460	470	480	
00-1	LKVL	SKRW	TM	YFKA	SYPSQ	LELS	EQDFLELA
99-1	LKVL	SKRW	AM	YFKA	SYPSQ	LELS	VQDFLELA
	490						
00-1	KRLI	WSVYPKNYLPE	IKN	499			
99-1	KKLI	WSVYPKNYLPE	IKN	499			

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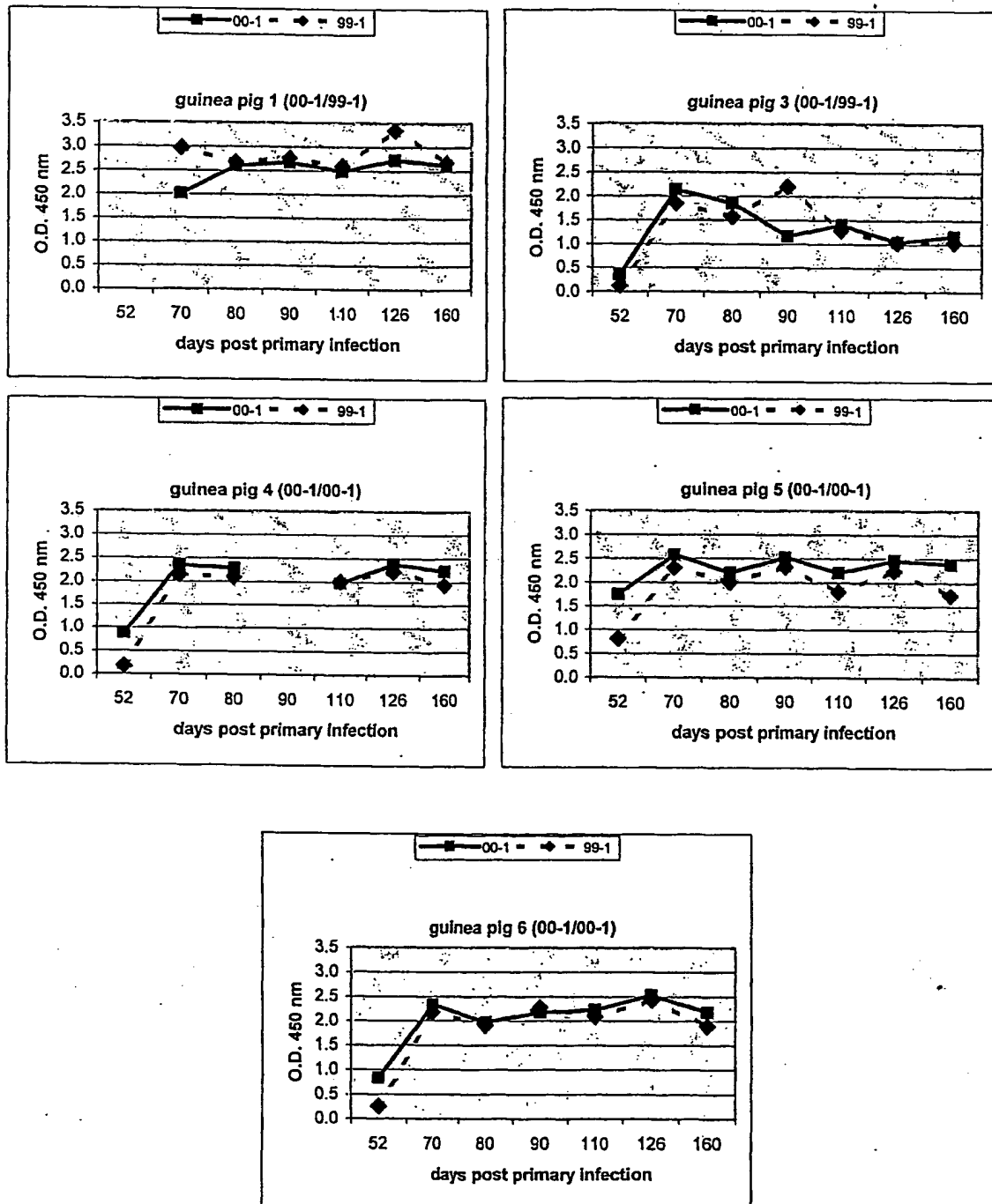
Fig. 29

+ = positive; - = negative; T = throatswabs; NO = nose swab; N = not done; ? = not sure;  
D = dead; 0 to 12: days post infection. 2e infection is only tested on nose swabs.

nr	1 <sup>e</sup> infection	swab	0	1	2	3	4	5	8	10	11	12	2 <sup>e</sup> infection	0	1	2	3	4	5
1	00-1	T	-	+	+	+	-	+	+	+	-	-	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
2	00-1	T	-	+	+	+	+	+	-	-	-	D		N	N	N	N	N	N
		NO		+	+	+	+	+	N	+	-	D		-	-	-	-	-	-
3	00-1	T	-	-	?	-	-	-	-	-	-	N	99-1	N	N	?	N	N	N
		NO		+	?	?		-	N	-	-	-		-	-	?	+	+	-
4	00-1	T	-	+	+	+	+	+	-	?	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	?	-	-		-	-	-	+	-	-
5	00-1	T	-	?	+	+	+	+	+	+	-	N	00-1	N	N	N	N	N	N
		NO		+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
6	00-1	T	-	-	+	+	+	+	-	+	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	+	?		-	-	-	-	-	-
7	99-1	T	-	-	-	+	+	-	+	D	-	-		N	N	N	N	N	N
		NO	-	-	-	+	+	+	N	D	-	-		-	-	-	-	-	-
8	99-1	T	-	-	+	+	-	-	-	-	-	N	00-1	N	N	N	N	N	N
		NO	-	?	-	+	+	?	N	-	-	-		-	-	+	+	+	+
9	99-1	T	-	-	-	-	-	-	-	-	-	N	00-1	N	N	N	N	N	N
		NO	-	-	-	-	+	+	N	-	-	-		-	?	+	+	-	-
10	99-1	T	-	-	-	+	+	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-	-		-	-	-	-	-	-
11	99-1	T	-	-	+	+	+	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	?	+	+	+	N	-	-	-		-	-	-	+	-	-
12	99-1	T	-	-	+	+	?	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-	-		-	-	-	-	-	-

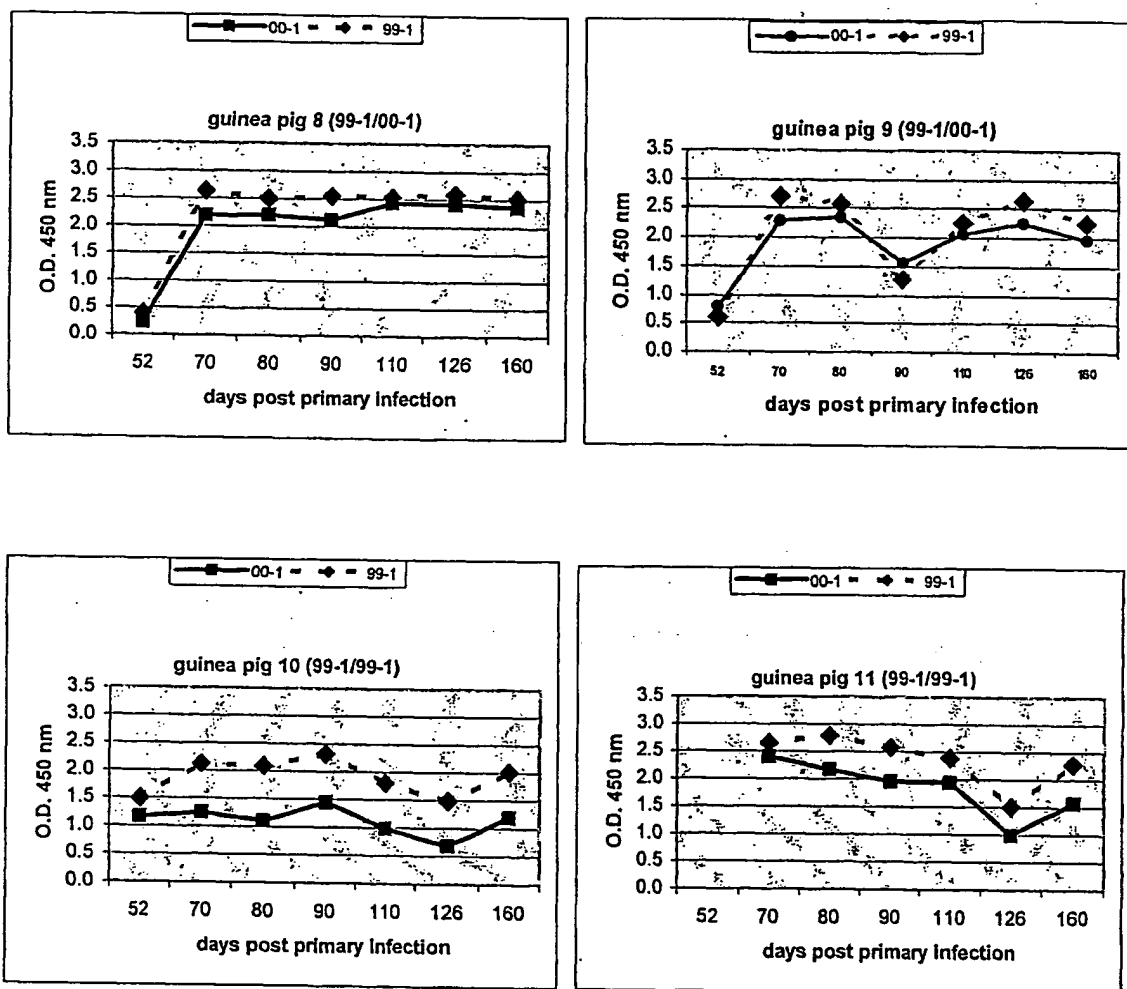
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Fig. 30A



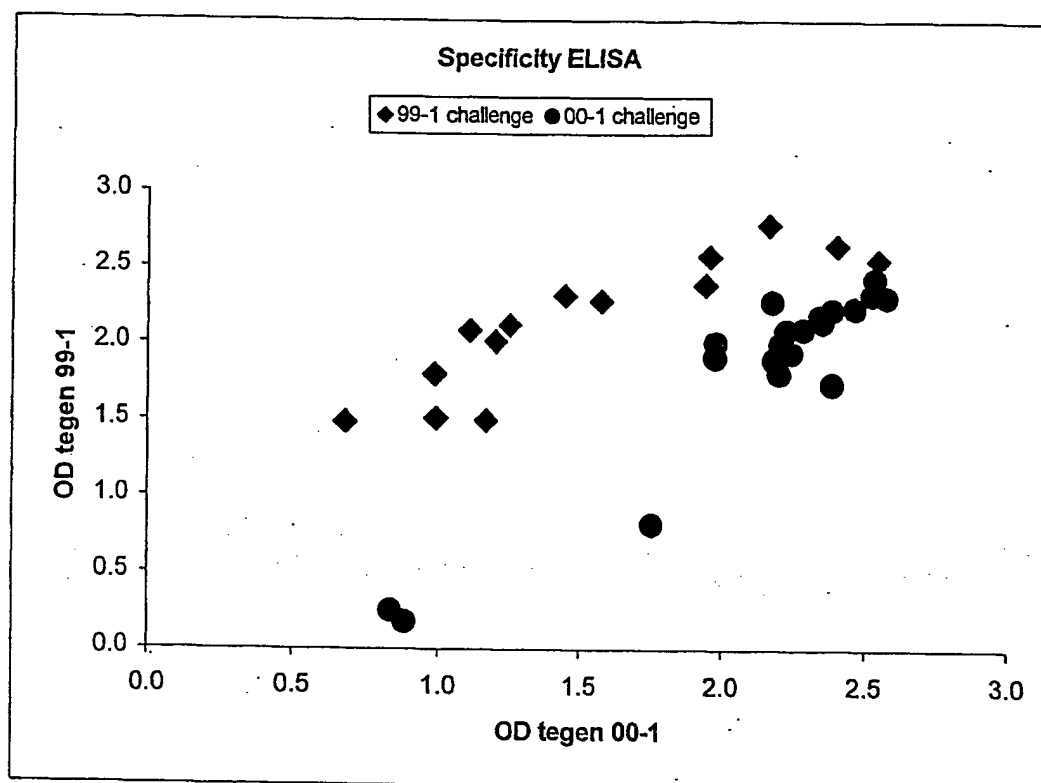
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Fig. 30B



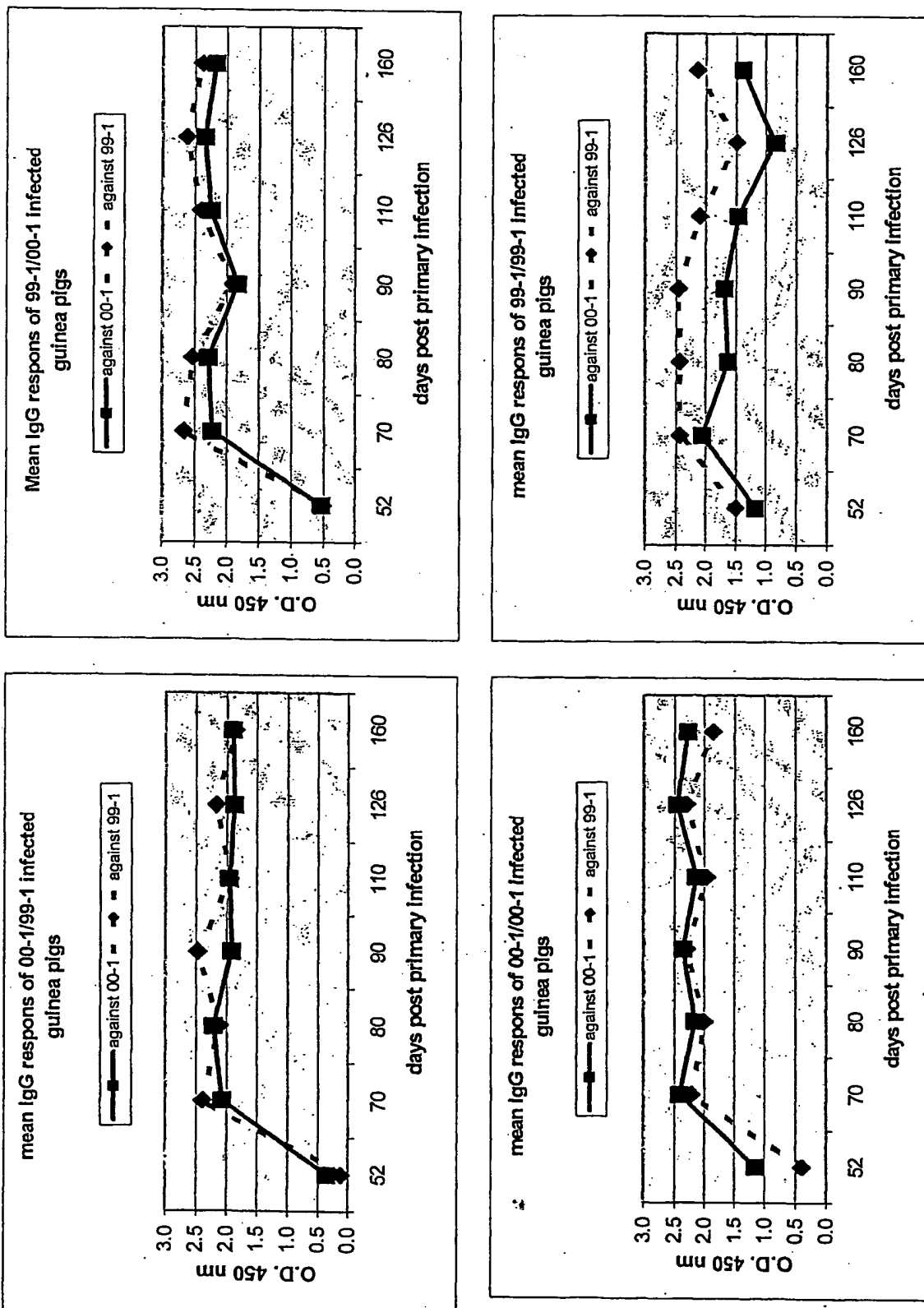
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Fig. 31



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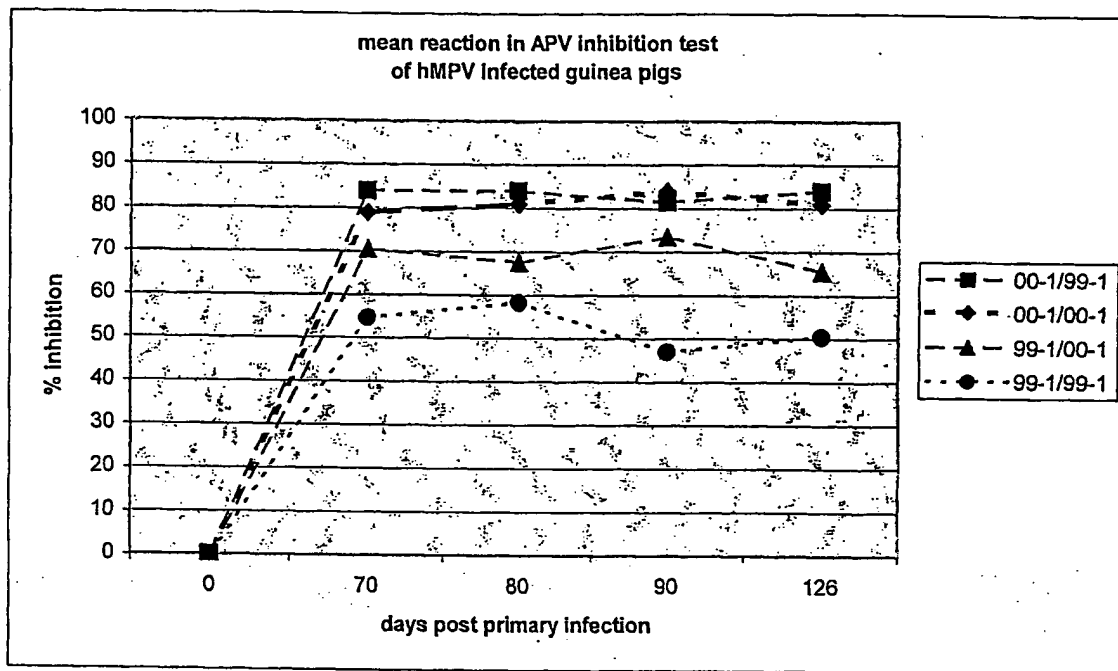
Fig. 32





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Fig. 33



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Fig. 34

	Against 00-1	Against 99-1	Against APV-C
1 infection with 00-1			
2 infections with 00-1			
1 infection with 99-1			
2 infections with 00-1			

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Fig. 35

+ = positive; - = negative; N = not done; ? = not sure; 0 to 10: days post infection

nr	1 <sup>st</sup> infection	0	2	3	4	5	6	7	8	9	11	2 <sup>nd</sup> infect ion	0	1	2	3	4	5	7	10
3	00-1	-	-	-	+	+	+	+	+	N	-		-	+	+	+	+	-	?	-
6	00-1	-	+	+	+	+	+	+	-	-	-		-	+	+	+	+	+	-	-

Fig. 36A

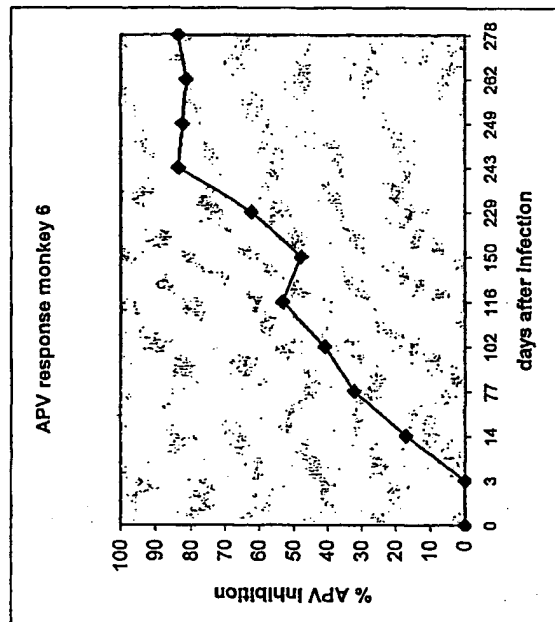
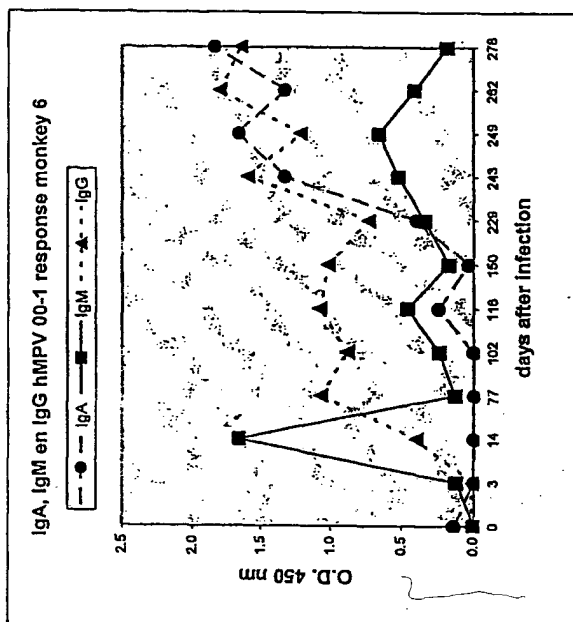
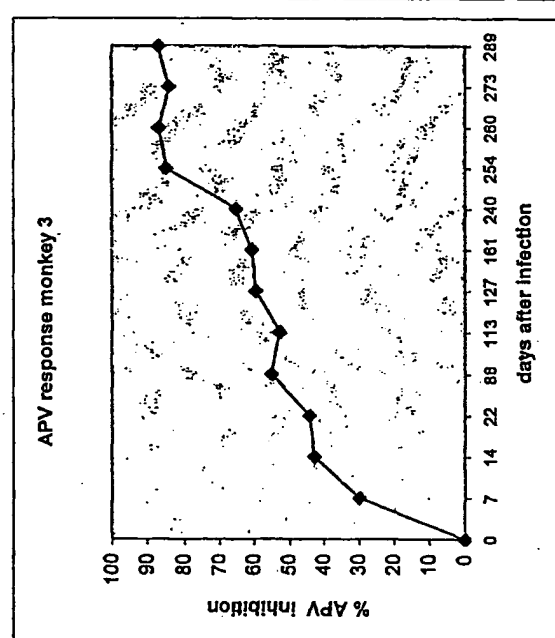
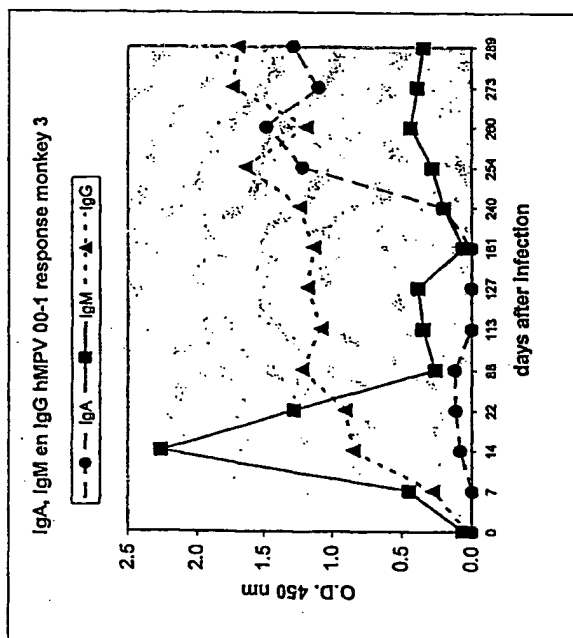


Fig. 36B



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Fig. 37

